

GenCore version 5.1.6
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 13, 2006, 16:16:04 ; Search time 27.947 Seconds
(without alignments)
1257.748 Million cell updates/sec

Title: US-10-801-517-2
Perfect score: 412
Sequence: 1 SDVYCVCFVLKVEVTKLID.....ILLEEVSPBLVCSMLHLCSSG 80

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*
1: Geneseq1980s.*
2: Geneseq1990s.*
3: Geneseq2000s.*
4: Geneseq2001s.*
5: Geneseq2002s.*
6: Geneseq2003as.*
7: Geneseq2003bs.*
8: Geneseq2004s.*
9: Geneseq2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	412	100.0	80	2	AAR70784 Saposin-C
2	412	100.0	80	2	AAR70784 Saposin-C
3	412	100.0	80	4	AAR70784 Saposin-C
4	412	100.0	80	7	AAR70784 Saposin-C
5	412	100.0	80	8	AAR70784 Saposin-C
6	412	100.0	80	8	AAR70784 Saposin-C
7	412	100.0	80	9	AAR70784 Saposin-C
8	412	100.0	80	9	AAR70784 Saposin-C
9	412	100.0	210	6	ABU05201 Human exp
10	412	100.0	385	6	ABR41750 Human pro
11	412	100.0	479	6	ABR39442 Human GEN
12	412	100.0	522	8	ADU24090 Human cys
13	412	100.0	523	4	ABR31916 Amino aci
14	412	100.0	523	6	ABU05211 Human exp
15	412	100.0	524	2	AAR70783 Prosapoin
16	412	100.0	524	2	AAR70783 Prosapoin
17	412	100.0	524	3	AAW85652 Human pro
18	412	100.0	524	6	ABU79099 Lip-TAA b
19	412	100.0	524	6	ABU05200 Human exp
20	412	100.0	524	6	ABU05207 Human exp
21	412	100.0	524	6	ABU05203 Human exp
22	412	100.0	524	6	ABU07340 Human exp
23	412	100.0	524	6	ABU05216 Human exp
24	412	100.0	524	6	ABU05202 Human exp

BEST AVAILABLE COPY

BEST AVAILABLE COPY

25	412	100.0	524	6	ABU05208 Human exp
26	412	100.0	524	6	ABU05214 Human exp
27	412	100.0	524	6	ABU05215 Human exp
28	412	100.0	524	6	ABU05199 Human exp
29	412	100.0	524	6	ABU05212 Human exp
30	412	100.0	524	6	ABU05213 Human exp
31	412	100.0	524	6	ABU05205 Human exp
32	412	100.0	524	7	ADJ43340 Superanti
33	412	100.0	524	7	ADJ69401 Human hea
34	412	100.0	524	8	ADO08060 Human pol
35	412	100.0	524	8	ADO94328 Human pre
36	412	100.0	524	8	ABM81149 Tumour-as
37	412	100.0	524	8	ADSR7894 Human pro
38	412	100.0	524	8	ADU48630 Human pro
39	412	100.0	524	9	ADW80727 Human pro
40	412	100.0	524	9	ADX06774 Cyclin-de
41	412	100.0	524	9	ADY14302 PRO poly
42	412	100.0	526	6	ABU05209 Human exp
43	412	100.0	527	4	ABR31915 Amino aci
44	412	100.0	527	5	ABP68602 Human pan
45	412	100.0	527	6	ABU79100 Lip-TAA b

ALIGNMENTS

RESULT 1
AAR70784
ID AAR70784 standard; protein; 80 AA.
XX
XX AAR70784;
XX AC
XX 25-MAR-2003 (revised)
DT 30-AUG-1995 (first entry)
XX
XX Saposin-C.
XX
XX Saposin-C; neuron; myelination; nervous system; neuroblastoma;
KW neurotrophic peptide; multiple sclerosis; leukoencephalitis;
KW adrenal leukodystrophy.
XX
XX Homo sapiens.
XX
XX WO9503821-A1.
XX
XX 09-FEB-1995.
XX
XX 28-JUL-1994; 94WO-US008453.
XX
XX 30-JUL-1993; 93US-00100247.
XX 21-APR-1994; 94US-00232513.
PA (OBRI/) O'BRIEN J S.
XX
XX O'Brien JS, Kishimoto Y;
WPI; 1995-082029/11.
XX
XX Stimulating neural cell out-growth and myelination - with pro:saposin,
PT saposin C or new neurotrophic peptide(s) from cytokine(s), for treating
PT nervous system diseases.
XX
XX Disclosure; Page 32; 50pp; English.
XX
XX The peptide given in AAR70773, corresponding to amino acids 8-29 of human
CC saposin-C (AAR70784), promotes neurite outgrowth in vitro. A consensus
CC sequence was determined by comparing the peptide with hematopoietic and
CC neuropoietic cytokines, and neurotrophic peptides (AAR70774-82) were
CC identified in the AB loop of human ciliary neurotrophic factor,
CC interleukin-6, -2, -3 and -gamma, erythropoietin and leukocyte
CC inhibitory factor, and in helix C of human interleukin-1-beta and
CC oncostatin-M. Prosapoin (AAR70783) and saposin-C also promoted nerve
CC cell myelination ex vivo. (Updated on 25-MAR-2003 to correct PN field.)

CC (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to
 CC correct PI field.)
 XX
 SQ Sequence 80 AA;
 Query Match 100.0%; Score 412; DB 2; Length 80;
 Best Local Similarity 100.0%; Pred. No. 2.4e-40;
 Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDKMCCKLPKSLSECEQVVDVTYSSILS 60
 DB 1 SDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDKMCCKLPKSLSECEQVVDVTYSSILS 60
 QY 61 ILLEEVSPELVCSMLHLCSSG 80
 DB 61 ILLEEVSPELVCSMLHLCSSG 80
 RESULT 2
 ID AAW85653 standard; peptide; 80 AA.
 XX
 AC AAW85653;
 XX
 DT 19-JUL-1999 (first entry)
 XX
 DE Human saposin C.
 XX
 KW Prosaposin, saposin; prosaptides; prosaposin receptor agonists; PRA;
 KW peripheral nervous system; central nervous system; PNS; CNS; Akt; Bcl-2;
 KW therapy; treatment; apoptosis; caspase; tumour necrosis factor; TNF;
 KW cytokine; interferon gamma; IFN; inflammation; rheumatoid arthritis;
 KW Crohn's disease; irritable bowel syndrome; asthma; cardiac infarction;
 KW congestive heart failure; multiple sclerosis;
 KW acute disseminated inflammatory leukoencephalitis;
 KW progressive multifocal leukoencephalitis; Alzheimer's disease;
 KW Parkinson's disease; amyotrophic lateral sclerosis; Huntington's disease;
 KW ischemic heart disease; Guillain-Barre disease; alopecia; AIDS dementia;
 KW cerebral malaria; HTLV; neuropathy;
 KW inflammatory neurodegenerative disease; toxin-induced liver disease.
 XX
 OS Homo sapiens.
 XX
 PN WO9912559-A1.
 XX
 PD 18-MAR-1999.
 XX
 PF 09-SEP-1998; 98WO-US019216.
 XX
 PR 09-SEP-1997; 97US-0058352P.
 PR 04-JUN-1998; 98US-0088129P.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI O'brien JS;
 XX
 DR WPI; 1999-229139/19.
 XX
 XX Use of prosaposin receptor agonist.
 XX
 PS Claim 7; Fig 2; 90pp; English.
 XX
 CC Prosaposin is a 70kDa glycoprotein which is proteolytically processed to
 CC generate saposins A, B, C and D, all of which are similar to each other
 CC and have a similar placement of six cysteines, a glycosylation site and
 CC conserved proline residues. Prosaposin, saposin C and prosaposin derived
 CC peptides (prosaptides), have therapeutic applications in promoting
 CC recovery after toxic, traumatic, myocardial ischaemic, degenerative and
 CC inherited lesions to the peripheral and central nervous system.
 CC Prosaposin receptor agonists (PRA) inhibit proinflammatory cytokine-
 CC induced apoptosis by activation of the Ser/Thr protein kinase Akt. Akt
 CC dissociates complexes of Bcl-2 family members, such as BAD-Bcl-2,
 CC releasing Bcl-2 and its family members which inhibit caspases, thereby

CC inhibiting apoptosis. An additional mechanism whereby PRA inhibit
 CC apoptosis is by blocking activation of JNK, a proapoptotic signaling
 CC component. Within several minutes after binding to the receptor, PRA
 CC block JNK activation induced by tumor necrosis factor-alpha (TNF alpha).
 CC The activation of JNK by TNF alpha is another well known mechanism for
 CC TNF alpha-induced, as well as other proinflammatory cytokine-induced
 CC apoptosis. The method can be used for inhibiting apoptosis which is
 CC caspase-mediated or induced by a proinflammatory cytokine, for example
 CC TNF alpha or interferon-gamma. It can be used for inhibiting apoptosis
 CC associated with a disorder such as e.g. rheumatoid arthritis, Crohn's
 CC disease, irritable bowel syndrome, asthma, cardiac infarction, congestive
 CC heart failure, multiple sclerosis, acute disseminated inflammatory
 CC leukoencephalitis, progressive multifocal leukoencephalitis, Alzheimer's
 CC disease, Parkinson's disease, amyotrophic lateral sclerosis, Huntington's
 CC disease, ischemic heart disease, Guillain-Barre disease, traumatic brain
 CC injury, traumatic spinal cord injury, alopecia, AIDS dementia, cerebral
 CC malaria, HTLV, neuropathy, inflammatory neurodegenerative disease, and
 CC toxin-induced liver disease. Saposin C acts as a prosaposin receptor
 CC agonist
 XX
 SQ Sequence 80 AA;
 Query Match 100.0%; Score 412; DB 2; Length 80;
 Best Local Similarity 100.0%; Pred. No. 2.4e-40;
 Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDKMCCKLPKSLSECEQVVDVTYSSILS 60
 DB 1 SDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDKMCCKLPKSLSECEQVVDVTYSSILS 60
 QY 61 ILLEEVSPELVCSMLHLCSSG 80
 DB 61 ILLEEVSPELVCSMLHLCSSG 80
 RESULT 3
 ID AAU05697 standard; protein; 80 AA.
 XX
 AC AAU05697;
 XX
 DT 24-OCT-2001 (first entry)
 XX
 DE Human Saponin C, SapC.
 XX
 KW Human; glucocerebrosidase; GCB; lysosomal storage disease;
 KW Gaucher's disease; Fabry's disease; Farber's disease;
 KW G_m_1 gangliosidosis; Tay-Sach's disease; Niemann-Pick disease;
 KW Shindler disease; Hunter syndrome; Sly syndrome; Huler syndrome;
 KW Scheie syndrome; Saponin C; SapC.
 XX
 OS Homo sapiens.
 XX
 PN WO200149830-A2.
 XX
 PD 12-JUL-2001.
 XX
 PF 29-DEC-2000; 2000WO-DK000743.
 XX
 PR 30-DEC-1999; 99DK-00001891.
 PR 02-JUN-2000; 2000DK-0000865.
 PR 02-JUN-2000; 2000DK-00000866.
 PR 30-JUN-2000; 2000DK-00001027.
 XX
 PA (MAXY-) MAXYGEN APS.
 XX
 PI Okkels JS, Jensen AD, Halkier T, Jensen RB, Schambye HT;
 XX WPI; 2001-465259/50.
 XX
 PT Improved lysosomal enzymes and lysosomal enzyme activators useful for
 PT treating Gaucher's disease.
 XX

PS Example 5; Page 96; 97pp; English.

XX The sequence represents human Saponin C (SapC), an essential co-factor
 CC for the lysosomal enzyme glucocerebrosidase. GCB. GCB is the enzyme
 CC involved in Gaucher's disease, a lysosomal storage disease. The invention
 CC relates to introducing new glycosylation sites into lysosomal
 CC enzymes/activators like GCB to improve their bioactivity. The novel
 CC polypeptides are used for the prevention and treatment of Gaucher's
 CC disease, Fabry's disease, Farber's disease, G.M.1 gangliosidosis, Tay-
 CC Sach's disease, Niemann-Pick disease, Shindler disease, Hunter syndrome,
 CC Sly syndrome, Hurler and Huler/Scheie syndromes

XX Sequence 80 AA;

Query Match 100.0%; Score 412; DB 4; Length 80;
 Best Local Similarity 100.0%; Pred. No. 2.4e-40;
 Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SDVYCEVCEFLVKEVTKLIDNNKTEKELIDAFDKMCKSLPKSLSECOEVVDITYGSSILS 60
 Db 1 SDVYCEVCEFLVKEVTKLIDNNKTEKELIDAFDKMCKSLPKSLSECOEVVDITYGSSILS 60

Qy 61 ILLEVSPELVCSMLHLCSSG 80
 Db 61 ILLEVSPELVCSMLHLCSSG 80

RESULT 4

ABU63252
 ID ABU62252 standard; protein; 80 AA.

XX AC ABU62252;

XX 29-AUG-2003 (first entry)

XX Spingolipid activator protein C (saposin C).

XX Spingolipid activator protein; saposin; neuroprotective; human;
 KW gene therapy; anionic phospholipid; fusogenic protein; prosaposin;
 KW Gauchers disease; saposin C.

XX Homo sapiens.

XX US2003095999-A1.

XX 22-MAY-2003.

XX 09-FEB-2001; 2001US-00780438.

XX 11-FEB-2000; 2000US-0181754P.

XX (Q1XX/) Q1 X.

XX Q1 X;

XX WPI; 2003-512933/48.

XX Delivering pharmaceutical agent through membrane used for treating

PT Gauchers disease, by applying composition comprising anionic
 PT phospholipids and fusogenic protein derived from prosaposin in carrier to
 PT membrane.

XX Disclosure; Fig 4; 19pp; English.

XX The invention describes a method of delivering a pharmaceutical agent
 CC through a membrane comprising applying to the membrane a composition (I)
 CC comprising: (1) anionic phospholipids; (2) a pharmaceutical agent
 CC contained within the phospholipids; and (3) a fusogenic protein or
 CC polypeptide derived from prosaposin in a carrier. The method can be used
 CC for delivering pharmaceutical agents through a biological membrane in
 CC cosmetic and medicinal applications, particularly for treating Gauchers
 CC disease. This is the amino acid sequence of sphingolipid activator
 CC protein C (saposin C) for use in the delivery composition

XX Sequence 80 AA;

Query Match 100.0%; Score 412; DB 7; Length 80;
 Best Local Similarity 100.0%; Pred. No. 2.4e-40;
 Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SDVYCEVCEFLVKEVTKLIDNNKTEKELIDAFDKMCKSLPKSLSECOEVVDITYGSSILS 60
 Db 1 SDVYCEVCEFLVKEVTKLIDNNKTEKELIDAFDKMCKSLPKSLSECOEVVDITYGSSILS 60

Qy 61 ILLEVSPELVCSMLHLCSSG 80
 Db 61 ILLEVSPELVCSMLHLCSSG 80

RESULT 5

ADQ94329
 ID ADQ94329 standard; protein; 80 AA.

XX AC ADQ94329;

XX 23-SEP-2004 (first entry)

XX Human Prosaposin protein, C-domain.

XX Human; prosaposin; C-domain; prosaposin receptor agonist;
 KW neuropathic pain; neurite outgrowth; neural cell death; myelination;
 KW demyelination; neuropathy; peripheral nerve disorder; neuroma;
 KW nerve compression; nerve crush; nerve stretch;
 KW incomplete nerve transection; mononeuropathy; polyneuropathy.

XX Homo sapiens.

XX US2004121958-A1.

XX 24-JUN-2004.

XX 24-DEC-2003; 2003US-00746442.

XX 05-MAR-1996; 96US-00611307.

XX 05-MAR-1997; 97WO-US004143.

XX 11-SEP-1997; 97US-00928074.

XX (REGC) UNIV CALIFORNIA.

XX O'brien JS;

XX WPI; 2004-468194/44.

XX New prosaposin receptor agonist, useful in alleviating or treating
 PT neuropathic pain, inhibiting the onset of neuropathic pain, neural cell
 PT death, demyelination, or sensory or motor neuropathy, and stimulating
 PT neurite outgrowth.

XX Disclosure; SEQ ID NO 24; 33pp; English.

XX The invention relates to a prosaposin receptor agonist comprising a
 CC defined amino acid sequence of 14-50 amino acids conforming to the
 CC consensus sequence appearing as ADQ94330. The agonists are based on
 CC peptides derived from the C domain of human prosaposin (or homologous
 CC peptides from other proteins). Also included are a pharmaceutical
 CC composition comprising the prosaposin receptor agonist in a
 CC pharmaceutical carrier, a method of alleviating neuropathic pain in a
 CC subject, a method of inhibiting the onset of neuropathic pain in a
 CC subject, a method of stimulating neurite outgrowth (or inhibiting neural
 CC cell death, promoting myelination or inhibiting demyelination) and a
 CC method of inhibiting sensory or motor neuropathy. The neuropathic pain
 CC results from a peripheral nerve disorder, e.g. neuroma, nerve
 CC compression, nerve crush, nerve stretch and incomplete nerve
 CC transection, mononeuropathy or polyneuropathy or results from a disorder
 CC of dorsal root ganglia, spinal cord, brainstem, thalamus, or cortex. The
 CC prosaposin receptor agonist, composition, and methods are useful in

us-10-801-517-2.rag

Wed Jan 18 11:58:41 2006

CC The subject is a mammal, preferably a human. The cell death preferably
 CC occurs through apoptosis. The agent is useful in treating cancer by
 CC inducing cell death in hyperproliferating cells. The present sequence
 CC represents a human Saposin C polypeptide.

XX Sequence 80 AA;
 SQ Query Match 100.0%; Score 412; DB 8; Length 80;
 Best Local Similarity 100.0%; Pred. No. 2.4e-40;
 Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDKMCCKLPSLSECEQVVDVTYSSILS 60
 Db 1 SDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDKMCCKLPSLSECEQVVDVTYSSILS 60

Qy 61 ILLEEVSPELVCSMLHLCSSG 80
 Db 61 ILLEEVSPELVCSMLHLCSSG 80

RESULT 7
 ADW80728
 ID ADW80728 standard; protein; 80 AA.

XX ADW80728;
 AC ADW80728;
 DT 07-APR-2005 (first entry)
 XX Human saposin C, SEQ ID NO:24.

DE Pharmaceutical; neuropathy; analgesic; antidiabetic; cell death;
 XX diabetes; neurological disease; neuropathic pain; saposin C.
 KW Homo sapiens.
 OS Homo sapiens.

XX US6849602-B1.
 XX 01-FEB-2005.
 XX 11-SEP-1997; 97US-00928074.
 XX 05-MAR-1996; 96US-00611307.
 XX 05-MAR-1997; 97WO-US004143.
 XX (REGC) UNIV CALIFORNIA.

XX Obrien JS;
 XX WPI; 2005-129968/14.

XX New pharmaceutical composition comprising a prosaposin receptor agonist
 PT and a carrier, where the composition is in a controlled release,
 PT liposomal or unit dosage form, useful for alleviating neuropathic pain
 PT resulting from diabetes.

XX Disclosure; SEQ ID NO 24; 35pp; English.

XX The invention relates to pharmaceutical composition comprising a
 CC prosaposin receptor agonist and a carrier, where the composition is in a
 CC controlled release, liposomal or unit dosage form. The invention also
 CC relates to prosaposin receptor agonists and the use of these agonists for
 CC stimulating neurite outgrowth, inhibiting neural cell death, promoting
 CC myelination, inhibiting neural demyelination and inhibiting sensory or
 CC motor neuropathy. The pharmaceutical composition is useful for
 CC alleviating neuropathic pain resulting from diabetes. The present
 CC sequence is human saposin C, which is derived from prosaposin. Note: The
 CC present sequence is given in the sequence listing, but is not further
 CC referred to in the specification.

XX Sequence 80 AA;
 SQ Query Match 100.0%; Score 412; DB 9; Length 80;
 Best Local Similarity 100.0%; Pred. No. 2.4e-40;

CC alleviating or treating neuropathic pain, inhibiting the onset of
 CC neuropathic pain, neural cell death, demyelination, or sensory or motor
 CC neuropathy, and in stimulating neurite outgrowth. The present sequence
 CC represents the C-domain of Human prosaposin.

XX Sequence 80 AA;
 SQ Query Match 100.0%; Score 412; DB 8; Length 80;
 Best Local Similarity 100.0%; Pred. No. 2.4e-40;
 Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDKMCCKLPSLSECEQVVDVTYSSILS 60
 Db 1 SDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDKMCCKLPSLSECEQVVDVTYSSILS 60

Qy 61 ILLEEVSPELVCSMLHLCSSG 80
 Db 61 ILLEEVSPELVCSMLHLCSSG 80

RESULT 6
 ADU48631
 ID ADU48631 standard; protein; 80 AA.

XX ADU48631;
 AC ADU48631;
 DT 27-JAN-2005 (first entry)
 XX Human Saposin C polypeptide.

DE Prosaposin; saposin C; phosphatidylserine; dioleoylphosphatidylserine;
 XX cytosolic; apoptosis stimulator; human.

XX Homo sapiens.
 OS Homo sapiens.

XX WO2004096159-A2.
 XX 11-NOV-2004.

XX 17-MAR-2004; 2004WO-US008020.
 XX 28-APR-2003; 2003US-0466166P.
 XX 16-MAR-2004; 2004US-00801517.

XX (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.

XX Q1 X;

XX WPI; 2004-804606/79.

XX New agent comprising an inner leaflet component (preferably
 PT phosphatidylserine) and a prosaposin-related polypeptide with plasma
 PT membrane affinity comprising a sequence of 524 or 80 amino acids, useful
 PT in treating cancer.

XX Claim 1; SEQ ID NO 2; 53pp; English.

XX The invention relates to a agent comprising an inner leaflet component
 CC and a prosaposin-related polypeptide. The prosaposin-related polypeptide
 CC is selected from ADU48630 or ADU48631, where the polypeptide retains
 CC plasma-membrane affinity. The inner leaflet component is
 CC phosphatidylserine or its structural analogue, and is especially
 CC dioleoylphosphatidylserine. The agent promotes cell death in
 CC hyperproliferating cells (tumour cells and cancer cells). The agent can
 CC be used in a method (M1) for modulating the distribution of an inner
 CC leaflet component in a plasma membrane of a cell of a subject; modulating
 CC (M2) tumour volume in a subject; treating (M3) cancer in a subject. In M1
 CC the concentration of the inner leaflet component in the outer leaflet of
 CC the plasma membrane is altered (preferably increased). The distribution
 CC of the inner leaflet component is modulated in hyper-proliferating cells
 CC (tumour cells and cancer cells). In M2 and M3 the agent promotes cell
 CC death in hyperproliferating cells which are preferably selected from
 CC sarcoma, neuroblastoma, breast carcinoma, and squamous carcinoma cells.

Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDKMCCKLPKSLSECEQVVDYTGSSILS 60
|||||
Db 1 SDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDKMCCKLPKSLSECEQVVDYTGSSILS 60
|||||

QY 61 ILLEEVSPELVCSMLHLCSSG 80
|||||
Db 61 ILLEEVSPELVCSMLHLCSSG 80
|||||

RESULT 8
ADZ88479
ID ADZ88479 standard; protein; 80 AA.

XX AC

XX AC

DT 14-JUL-2005 (first entry)

XX Human saposin C fusogenic protein.

XX Saposin C; pharmaceutical; drug delivery; cosmetics; gauchers disease;
KW metabolic; neurological disease; beta-glucosidase activator;
KW sphingolipid activator protein.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Binding-site 3..15 /note= "lipid binding region"

FT Region 4..19 /note= "Helix 1"

FT Disulfide-bond 5..78

FT Disulfide-bond 8..72

FT Region 17..33 /note= "Neuritogenic region"

FT Region 25..40 /note= "Helix 2"

FT Disulfide-bond 36..47

FT Region 43..61 /note= "Helix 3"

FT Active-site 46..61 /note= "Beta-glucosidase activation region"

FT Region 63..80 /note= "Helix 4"

FT Binding-site 65..76 /note= "lipid binding region"

FT US2005100591-A1. (10/967,921)

XX 12-MAY-2005.

XX 18-OCT-2004; 2004US-00967921.

XX 11-FEB-2000; 2000US-0181754P.

XX 09-FEB-2001; 2001US-00780438.

XX (Q1XX/) Q1 X.

XX Q1 X;

XX WPI; 2005-345361/35.

XX Delivering a pharmaceutical agent through a dermal or mucosal membrane to
PT e.g. treat Gaucher's disease, comprises applying to the membrane a
PT composition comprising a fusogenic protein, such as saposin C.
XX Disclosure; Fig 4; 26pp; English.

XX The present invention relates to methods of delivering pharmaceutical
CC agents across biological membranes where the pharmaceutical agent is
CC contained within the phospholipid membrane and delivery is facilitated by
CC a membrane fusogenic protein, saposin, derived from prosaposin. Saposins

CC are sphingolipid activator proteins or coenzymes that also promotes acid
CC beta-glucosidase activity by inducing the enzyme conformational change at
CC acidic pH. The methods and composition of the invention are useful for
CC enhancing the transport and delivery of pharmaceutical agents across
CC and/or within dermal and mucosal membranes for both cosmetic and
CC medicinal applications such as in treating Gaucher's disease. The present
CC sequence is human saposin C fusogenic protein.

XX Sequence 80 AA;

Query Match 100.0%; Score 412; DB 9; Length 80;

Best Local Similarity 100.0%; Pred. No. 2.4e-40;

Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDKMCCKLPKSLSECEQVVDYTGSSILS 60
|||||

Db 1 SDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDKMCCKLPKSLSECEQVVDYTGSSILS 60
|||||

QY 61 ILLEEVSPELVCSMLHLCSSG 80
|||||

Db 61 ILLEEVSPELVCSMLHLCSSG 80
|||||

RESULT 9

ABU05201

ID ABU05201 standard; protein; 210 AA.

XX AC

XX AC

DT 29-JAN-2003 (first entry)

XX Human expressed protein tag (EPT) #1867.

XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.

XX Homo sapiens.

XX WO200278524-A2.

XX 10-OCT-2002.

XX 28-MAR-2002; 2002WO-US009671.

XX 28-MAR-2001; 2001US-0279495P.

XX 21-MAY-2001; 2001US-0292544P.

XX 08-AUG-2001; 2001US-0310801P.

XX 01-OCT-2001; 2001US-0326370P.

XX 04-DEC-2001; 2001US-0336780P.

XX 20-FEB-2002; 2002US-0358985P.

XX (ZYCO-) ZYCOS INC.

XX Chicx RM, Tomlinson AJ, Urban RG;

XX WPI; 2003-040607/03.

XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.

XX Example 2; SEQ ID NO 1867; 134pp; English.

XX The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this

Wed Jan 18 11:58:41 2006

CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 210 AA;
Query Match 100.0%; Score 412; DB 6; Length 210;
Best Local Similarity 100.0%; Pred. No. 8.6e-40; Indels 0; Gaps 0;
Matches 80; Conservative 0; Mismatches 0;
QY 1 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDADFDMCKSLPKSLSECEQVVDVTYGSILS 60
DB 8 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDADFDMCKSLPKSLSECEQVVDVTYGSILS 67
QY 61 ILLEEVSPELVCSMLHLCSG 80
DB 68 ILLEEVSPELVCSMLHLCSG 87
RESULT 10
ABR41750
ID ABR41750 standard; protein; 385 AA.
XX ABR41750;
XX 02-JUN-2003 (first entry)
XX Human DITHP biochemical pathway protein.
XX Human; dithp; diagnostic and therapeutic polynucleotide; diagnosis;
KW cancer; cell proliferative disorder; autoimmune disorder;
KW inflammatory disorder; infection; hormonal disorder; metabolic disorder;
KW neurological disorder; gastrointestinal disorder; transport disorder;
KW connective tissue disorder; drug screening; proteome analysis;
KW gene therapy; antisense therapy; genotyping; transgenic animal; knock in;
KW disease model; toxicological testing; transcript imaging;
KW biochemical pathway.
XX Homo sapiens.
XX WO200297031-A2.
XX 05-DEC-2002.
XX 27-MAR-2002; 2002WO-US010056.
XX 28-MAR-2001; 2001US-0279619P.
XX 29-MAR-2001; 2001US-0280067P.
XX 29-MAR-2001; 2001US-0280068P.
XX 16-MAY-2001; 2001US-0291280P.
XX 17-MAY-2001; 2001US-0291829P.
XX 17-MAY-2001; 2001US-0291849P.
XX 19-JUN-2001; 2001US-0295428P.
XX 20-JUN-2001; 2001US-0295776P.
XX 20-JUN-2001; 2001US-0300001P.
XX (INCY-) INCYTE GENOMICS INC.
XX Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;
XX Dufour GE, Hillman JL, Yu JY, Tuason O, Yap PE, Ameshey SR;
XX Daughtery SC, Dam TC, Liu TP, Nguyen DA, Kleefeld Y, Gerstin EH;
XX Peralta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;
XX Flores V, Marwaha R, Lo A, Lan RY, Urashka ME;
XX WPI; 2003-129518/12.
DR

DR N-PSDB; ACC46687.
XX Novel human diagnostic and therapeutic polypeptide useful for identifying
XX test compound which specifically binds to a polypeptide encoded by human
XX diagnostic and therapeutic polynucleotide, and to induce antibodies.
XX Claim 27; SEQ ID NO 1285; 591pp; English.
XX The invention relates to novel human diagnostic and therapeutic
XX polynucleotides designated dithp (ACC46080-ACC46749) and to their encoded
XX proteins (DITHP; ABR41136-ABR41812). The invention also relates to
XX polynucleotide sequences at least 90% identical to the dithp cDNA
XX sequences of the invention; recombinant vectors, host cells and
XX transgenic organisms comprising a dithp nucleic acid sequence; the
XX recombinant production of DITHP proteins; antibodies specific for DITHP
XX proteins; microarrays comprising dithp nucleic acid sequences; methods of
XX detecting dithp nucleotide and protein sequences; methods of screening
XX for compounds which specifically bind a DITHP protein; and methods of
XX assessing the toxicity of test compounds using a dithp hybridisation
XX probe. Dithp nucleic acid sequences and DITHP proteins may be used in the
XX diagnosis of a wide variety of conditions including cancer and other cell
XX proliferative disorders; autoimmune or inflammatory disorders; bacterial,
XX viral, fungal or parasitic infections; gastrointestinal disorders; transport
XX disorders; neurological disorders; gastrointestinal disorders; transport
XX disorders; and connective tissue activity or gene expression. DITHP
XX proteins can additionally be used in analysis of the proteome of a tissue
XX or cell type and to induce antibodies. The dithp nucleic acids are
XX additionally useful in somatic or germline gene therapy of the disorders
XX mentioned above, as a source of antisense sequences, as a source of
XX probes and primers, in genotyping and identification of individuals, in
XX the generation of transgenic animal models of human disease or knock in
XX humanised animals, in toxicological testing, and in transcript imaging.
XX The present sequence represents a DITHP protein which is involved in a
XX biochemical pathway. Note: The sequence data for this patent did not form
XX part of the printed specification, but was obtained in electronic format
XX directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 385 AA;
Query Match 100.0%; Score 412; DB 6; Length 385;
Best Local Similarity 100.0%; Pred. No. 1.9e-39; Indels 0; Gaps 0;
Matches 80; Conservative 0; Mismatches 0;
QY 1 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDADFDMCKSLPKSLSECEQVVDVTYGSILS 60
DB 172 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDADFDMCKSLPKSLSECEQVVDVTYGSILS 231
QY 61 ILLEEVSPELVCSMLHLCSG 80
DB 232 ILLEEVSPELVCSMLHLCSG 251
RESULT 11
ABR39442
ID ABR39442 standard; protein; 479 AA.
XX ABR39442;
XX 12-JUN-2003 (first entry)
XX Human GENSET polypeptide clone name SAP-MU-10.
XX GENSET; cytostatic; gene therapy; cancer; transgenic; human.
XX Homo sapiens.
XX WO2003014151-A2.
XX 20-FEB-2003.
XX 15-OCT-2001; 2001WO-IB002321.
XX

PR 10-AUG-2001; 2001US-0311305P.
 PR 24-AUG-2001; 2001US-03114734P.
 PR 07-SEP-2001; 2001US-0318204P.
 PR 01-OCT-2001; 2001US-0326470P.
 XX (GEST) GENSET SA.
 PA Bejanin S, Tanaka H;
 PI WPI; 2004-794441/78.
 XX Identifying compound that modulates activity of protease, by contacting
 DR protease with test compound, measuring activity of protease before and
 DR N-PSDB; ABZ76265.
 XX New GENSET gene, useful for preparing a composition for treating GENSET-
 PT related disorders.
 PT Claim 2; Page 288-289; 301pp; English.
 PS The invention relates to isolated GENSET polynucleotides and encoded
 CC polypeptides. The GENSET gene is useful for preparing a composition for
 CC treating GENSET-related disorders e.g., cancer. Sequences ABR39423-448
 CC represent the novel GENSET polypeptide sequences
 XX Sequence 479 AA;
 SQ
 Query Match 100.0%; Score 412; DB 6; Length 479;
 Best Local Similarity 100.0%; Pred. No. 2.5e-39;
 Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SDVYCEVCEFLVKVETKLDNNKTEKILDAFKMCKSLPKSLSECCQVVDYTGSSILS 60
 DB 314 SDVYCEVCEFLVKVETKLDNNKTEKILDAFKMCKSLPKSLSECCQVVDYTGSSILS 373
 QY 61 ILLEEVSPVLVCSMLHLCSG 80
 DB 374 ILLEEVSPVLVCSMLHLCSG 393
 RESULT 12
 ADU24090
 ID ADU24090 standard; protein; 522 AA.
 XX ADU24090;
 XX 27-JAN-2005 (first entry)
 DE Human cysteine peptidase enzyme #12.
 XX Protease; cancer; immune-related disorder; cardiovascular disease;
 KW brain-associated disease; neuronal-associated disease;
 KW metabolic disorder; haematopoietic; cytostatic; immunosuppressive;
 KW cardiovascular; cerebroprotective; neuroprotective; human;
 KW cysteine peptidase; enzyme; peripheral nervous system;
 KW Alzheimer's disease; Parkinson's disease; multiple sclerosis;
 KW amyotrophic lateral sclerosis; infection; ocular disease; migraine; pain;
 KW sexual dysfunction; mood disorder; attention disorder; cognition disorder;
 KW hypertension; hypotension; psychotic disorder; neurological disorder;
 KW dyskinesia; organ transplant rejection.
 OS Homo sapiens.
 XX Key Location/Qualifiers
 FH 258..444
 FT Domain /note = Protease active domain
 XX US2004219609-A1.
 PN 04-NOV-2004.
 XX 11-JUL-2003; 2003US-00618281.
 XX 12-JUL-2002; 2002US-0395325P.
 XX (DAYA/) DAY A G.

PA (ESTE/) ESTELL D A.
 PA (LYON/) LYONS E H.
 PA (YAO/) YAO J.
 XX Day AG, Estell DA, Lyons EH, Yao J;
 PI WPI; 2004-794441/78.
 XX Identifying compound that modulates activity of protease, by contacting
 DR protease with test compound, measuring activity of protease before and
 DR after contacting step, and determining whether test compound modulates
 PT activity of protease.
 PT Claim 1; SEQ ID NO 38; 206pp; English.
 PS The invention relates to a method for identifying a compound that
 CC modulates the activity of a protease, by contacting the protease with a
 CC test compound, measuring the activity of the protease before and after
 CC contacting step and determining whether test compound modulates the
 CC activity of the protease. The invention also relates to the proteins not
 CC previously identified as proteases. The method is useful for identifying
 CC a compound that modulates the activity of a protease. It is useful for
 CC treating a disease or disorder e.g., cancer, immune-related diseases and
 CC disorders, cardiovascular diseases, brain or neuronal-associated diseases
 CC or metabolic disorders (preferably cancer of tissue or haematopoietic
 CC origin) in mammal, preferably human. The method is also useful for
 CC treating diseases of the peripheral nervous system, Alzheimer's disease,
 CC Parkinson's disease, multiple sclerosis, amyotrophic lateral sclerosis,
 CC viral infections caused by prions, infections caused by bacteria and
 CC fungi, ocular diseases, migraines, pain, sexual dysfunction, mood
 CC disorders, attention disorders, cognition disorders, hypotension,
 CC hypertension, psychotic disorders, neurological disorders, dyskinesias
 CC and organ transplant rejection. The present sequence is the human
 CC cysteine peptidase, a novel protease enzyme.
 XX Sequence 522 AA;
 SQ
 Query Match 100.0%; Score 412; DB 8; Length 522;
 Best Local Similarity 100.0%; Pred. No. 2.8e-39;
 Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SDVYCEVCEFLVKVETKLDNNKTEKILDAFKMCKSLPKSLSECCQVVDYTGSSILS 60
 DB 309 SDVYCEVCEFLVKVETKLDNNKTEKILDAFKMCKSLPKSLSECCQVVDYTGSSILS 368
 QY 61 ILLEEVSPVLVCSMLHLCSG 80
 DB 369 ILLEEVSPVLVCSMLHLCSG 388
 RESULT 13
 AAB31916
 ID AAB31916 standard; protein; 523 AA.
 XX AAB31916;
 AC AAB31916;
 XX 15-MAY-2001 (first entry)
 DE Amino acid sequence of a human protein.
 XX Human; perlecan; retinol-binding plasma protein; calgranulin B; vaccine;
 KW ganglioside GM2 activator; saposin B; degenerative disease; glial cell;
 KW neurological disease; auto-immune disease; multiple sclerosis; toxicity;
 KW Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis;
 KW rheumatoid polyarthritis; lupus erythematosus; gene therapy.
 OS Homo sapiens.
 XX WO200105422-A2.
 PN 25-JAN-2001.
 XX 17-JUL-2000; 2000WO-FR002057.

us-10-801-517-2.rag

Wed Jan 18 11:58:41 2006

```

XX PR 15-JUL-1999; 99PR-00009372.
XX XX (INMR ) BIOMERIEUX STELHYS.
XX PA Roeklin D, Kolbe H, Charles M, Malcus C, Santoro L, Perron H;
XX PI WPI; 2001-159475/16.
XX XX
XX DR Detecting, preventing and treating degenerative, neurological and
XX PT autoimmune diseases, particularly multiple sclerosis, using specified
XX PT polypeptides or related nucleic acid or ligand.
XX XX
XX PS Claim 1; Page 174-175; 209pp; French.
XX XX
XX CC The present sequence represents a human protein, which is used in the
XX CC method of the invention. The specification describes a method which uses
XX CC at least one polypeptide or polynucleotide sequence belonging to the
XX CC perlecan, precursor of the retinol-binding plasma protein, precursor of
XX CC the ganglioside GM2 activator, calgranulin B or saposin B protein
XX CC families. The method is used for detecting, preventing or treating a
XX CC degenerative, neurological and/or auto-immune disease. The
XX CC polynucleotides and polypeptides are used for diagnosis, prognosis,
XX CC prevention and treatment of multiple sclerosis (in its various forms and
XX CC phases). They may also be useful in cases of e.g. Alzheimer's and
XX CC Parkinson's diseases, amyotrophic lateral sclerosis, rheumatoid
XX CC polyarthritis and lupus erythematosus, including use as vaccines and in
XX CC gene therapy (expression of sense or antisense sequences). They can also
XX CC be used to assess efficacy of potential therapeutic agents, particularly
XX CC compounds that reduce or inhibit toxicity towards glial cells
XX XX
XX SQ Sequence 523 AA;
XX Query Match 100.0%; Score 412; DB 4; Length 523;
XX Best Local Similarity 100.0%; Pred. No. 2.8e-39;
XX Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SDVCEVCEFLVKEVTKLIDNNKTEKILDAFDKMCCKLPKSLSECCQVVDYTGSSILS 60
Db 310 SDVCEVCEFLVKEVTKLIDNNKTEKILDAFDKMCCKLPKSLSECCQVVDYTGSSILS 369
QY 61 ILLEEVSPELVCSMLHLCSG 80
Db 370 ILLEEVSPELVCSMLHLCSG 389
RESULT 14
ABU05211
ID ABU05211 standard; protein; 523 AA.
XX AC ABU05211;
XX XX
XX DT 29-JAN-2003 (first entry)
XX DE Human expressed protein tag (BPT) #1877.
XX XX
XX KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
XX KW protease; protease inhibitor; transporter; cytoskeletal protein;
XX KW receptor; transcription factor; cancer; MHC;
XX KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
XX KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX OS Homo sapiens.
XX XX
XX PN WO200278524-A2.
XX XX
XX PD 10-OCT-2002.
XX XX
XX PF 28-MAR-2002; 2002WO-US009671.
XX PR 21-MAY-2001; 2001US-0279495P.
XX PR 21-MAY-2001; 2001US-0292544P.
XX PR 08-AUG-2001; 2001US-0310801P.
XX XX
XX PR 01-OCT-2001; 2001US-0326370P.
XX PR 04-DEC-2001; 2001US-0336780P.
XX PR 20-FEB-2002; 2002US-0358985P.
XX XX
XX PA (ZYCO-) ZYCOS INC.
XX XX
XX PI Chicz RM, Tomlinson AJ, Urban RG;
XX XX
XX DR WPI; 2003-040607/03.
XX XX
XX PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
XX PT cytoskeletal proteins, receptors or transcription factors), useful for
XX PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
XX PT leukemia.
XX XX
XX PS Example 2; SEQ ID NO 1877; 134pp; English.
XX XX
XX CC The invention describes a purified polypeptide, which comprises a
XX CC fragment of a kinase, phosphatase, protease, protease inhibitor,
XX CC transporter, cytoskeletal protein, receptor or transcription factor. The
XX CC polypeptide is useful as an immunogenic composition for eliciting in a
XX CC mammal an immunogenic response directed against any of the purified
XX CC polypeptide. The purified polypeptide, or the antibody that binds to this
XX CC polypeptide, is useful for treating cancer. The polypeptide is also
XX CC useful for identifying compounds that binds to a naturally processed
XX CC class I or class II MHC-binding polypeptide. The polypeptides and
XX CC polynucleotides are particularly useful for treating or preventing
XX CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
XX CC lymphoma or leukaemia. These are also useful for screening agents for
XX CC treating the above mentioned diseases. This sequence represents an
XX CC expressed protein tag (EPT) isolated from human tissue for translational
XX CC profiling. Note: This sequence does not appear in the printed from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX XX
XX SQ Sequence 523 AA;
XX Query Match 100.0%; Score 412; DB 6; Length 523;
XX Best Local Similarity 100.0%; Pred. No. 2.8e-39;
XX Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SDVCEVCEFLVKEVTKLIDNNKTEKILDAFDKMCCKLPKSLSECCQVVDYTGSSILS 60
Db 310 SDVCEVCEFLVKEVTKLIDNNKTEKILDAFDKMCCKLPKSLSECCQVVDYTGSSILS 369
QY 61 ILLEEVSPELVCSMLHLCSG 80
Db 370 ILLEEVSPELVCSMLHLCSG 389
RESULT 15
AAR70783
ID AAR70783 standard; protein; 524 AA.
XX AC AAR70783;
XX XX
XX DT 25-MAR-2003 (revised)
XX DT 30-AUG-1995 (first entry)
XX DE Prosaposin.
XX XX
XX KW Saposin-C; neuron; myelination; nervous system; neuroblastoma;
XX KW neurotrophic peptide; multiple sclerosis; leukoencephalitis;
XX KW adrenal leukodystrophy; prosaposin.
XX OS Homo sapiens.
XX XX
XX PN WO9503821-A1.
XX XX
XX PD 09-FEB-1995.
XX XX
XX PF 28-JUL-1994; 94WO-US008453.
XX XX

```


PR 30-JUL-1993; 93US-00100247.
XX 21-APR-1994; 94US-00232513.
PA (OBRI/) O'BRIEN J S.
XX O'brien JS, Kishimoto Y;
PI
XX WPI; 1995-082029/11.
DR N-PSDB; AAQ85355.
XX
PT Stimulating neural cell out-growth and myelination - with pro.saposin,
PT saposin C or new neurotrophic peptide(s) from cytokine(s), for treating
PT nervous system diseases.
XX
XX Disclosure; Page 30-32; 50pp; English.
XX
XX The peptide given in AAR70773, corresponding to amino acids 8-29 of human
CC saposin-C (AAR70784), promotes neurite outgrowth in vitro. A consensus
CC sequence was determined by comparing the peptide with hematopoietic and
CC neurotrophic cytokines, and neurotrophic peptides (AAR70774-82) were
CC identified in the AB loop of human ciliary neurotrophic factor,
CC interleukins-6, -2, -3 and -gamma, erythropoietin and leukocyte
CC inhibitory factor, and in helix C of human interleukin-1-beta and
CC oncostatin-M. Prosapoinin (AAR70783) and saposin-C also promoted nerve
CC cell myelination ex vivo. (Updated on 25-MAR-2003 to correct PN field.)
CC (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to
CC correct PI field.)
XX
SQ Sequence 524 AA;

Query Match 100.0%; Score 412; DB 2; Length 524;
Best Local Similarity 100.0%; Pred. No. 2.8e-39;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDMCKSLPKSLSECCQEVVDYTGSSILS 60
Db 311 SDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDMCKSLPKSLSECCQEVVDYTGSSILS 370

Qy 61 ILLEVSPELVCSMLHLCSG 80
Db 371 ILLEVSPELVCSMLHLCSG 390

Search completed: January 13, 2006, 16:30:19
Job time : 27.947 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.1.6
 Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 13, 2006, 16:22:54 ; Search time 30.4636 Seconds
 (without alignments)
 1852.779 Million cell updates/sec

Title: US-10-801-517-2
 Perfect score: 412
 Sequence: 1 SDVYCEVCEFLVKEVTKLID.....ILLREVSPELVCSMLHLCSG 80

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : UniProt_05.80.*
 1: uniprot_sprot.*
 2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	412	100.0	452	2	Q5R406 pongo pygma
2	412	100.0	524	1	P07602 h proactiva
3	412	100.0	524	2	Q53FJ5 homo sapien
4	412	100.0	524	2	Q5JQ36 homo sapien
5	412	100.0	527	2	Q5NVD5 pongo pygma
6	412	100.0	530	2	Q59EN5 homo sapien
7	412	100.0	559	2	Q5JQ37 homo sapien
8	405	98.3	526	2	Q5R4U7 pongo pygma
9	397	96.4	497	2	Q4R590 m brain cdn
10	346	84.0	525	1	P66779 b proactiva
11	261	63.3	81	1	SAP_CAVPO
12	210	51.0	512	2	Q7SY70 XENLA
13	207	50.2	550	2	Q4RQ38 TETNG
14	205	49.8	520	2	Q8UV24 BRARE
15	205	49.8	520	2	Q5P3G7 BRARE
16	205	49.8	520	2	Q5P3G7 BRARE
17	205	49.8	522	2	Q5P4H8 BRARE
18	203	49.3	518	1	SAP_CHICK
19	193	46.8	518	2	Q642S6 XENLA
20	193	46.8	553	2	Q6P7A4 RAT
21	193	46.8	554	1	SAP_RAT
22	171	41.5	200	2	Q75K05 DICDI
23	169	41.0	554	2	Q8BFQ1 MOUSE
24	169	41.0	557	1	SAP_MOUSE
25	164	39.8	522	2	Q54Q68 DICDI
26	163	39.6	336	2	Q54LG3 dictyosteli
27	158	38.3	965	2	Q15937 BOMMO
28	155	37.6	245	2	Q5ZL62 CHICK
29	153	37.1	238	2	Q5BZ62 SCHJA
30	153	37.1	922	2	Q5D981 SCHJA
31	150	36.4	876	2	Q8IMB4 drosophila

32 150 36.4 953 2 Q9Y125 DROME
 33 149.5 36.3 253 2 Q5R848 PONPY
 34 149 36.2 890 2 Q7PMW6 ANOGA
 35 147.5 35.8 241 2 Q8N7T4 HUMAN
 36 147.5 35.8 325 2 Q7PJB6 ANOGA
 37 147.5 35.8 478 2 Q7PJB7 ANOGA
 38 147.5 35.8 543 2 Q6NUJ1 HUMAN
 39 144 35.0 262 2 Q4SJ83 TETNG
 40 144 35.0 441 2 Q5U9P3 DROME
 41 143 34.7 240 2 Q5BJH1 HUMAN
 42 142 34.5 293 2 Q54PT7 DICDI
 43 141.5 34.3 402 2 Q8C1N0 MOUSE
 44 141.5 34.3 449 2 Q8BJV5 MOUSE
 45 141.5 34.3 525 2 Q8C1C1 MOUSE

ALIGNMENTS

RESULT 1
 Q5R406 PONPY PRELIMINARY; PRT; 452 AA.
 AC Q5R406;
 DT 01-FEB-2005 (TrEMBLrel. 29, Created)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
 DE Hypothetical protein DKFZp459G152.
 GN Name=DKFZp459G152;
 OS Pongo pygmaeus (Orangutan).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Pongo.
 OX NCBI_TaxID=9600;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Cortex;
 RG The German cDNA Consortium;
 RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Oeanger A.,
 RA Fobio G., Han M., Wiemann S.;
 RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; CR861454; CAH93510.1; -, mRNA.
 DR SMR; Q5R406; 119-200, 239-318.
 DR GO; GO:0005764; C:lysosome; IEA.
 DR GO; GO:0006629; P:lipid metabolism; IEA.
 DR GO; GO:0006665; P:sphingolipid metabolism; IEA.
 DR InterPro; IPR003119; Sapa.
 DR InterPro; IPR007856; Sapa.1.
 DR InterPro; IPR008138; Sapa.2.
 DR InterPro; IPR008140; Sapa_sub.
 DR InterPro; IPR008373; Saposin.
 DR InterPro; IPR008139; SaposinB.
 DR Pfam; PF02199; Sapa.1.
 DR Pfam; PF05184; Sapa.1; 4.
 DR Pfam; PF03489; Sapa.2; 4.
 DR PRINTS; PR01797; SAPOSIN.
 DR ProDom; PD001732; Sapa_sub; 2.
 DR SMART; SM00162; SAPA; 1.
 DR KW Hypothetical protein.
 SQ SEQUENCE 452 AA; 50664 MW; 6D30EAC665A399DD CRC64;

Query Match 100.0%; Score 412; DB 2; Length 452;
 Best Local Similarity 100.0%; Pred. No. 2.2e-30;
 Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SDVYCEVCEFLVKEVTKLIDNNKTEKILDAFQKCSKLPKSLSECEQVVDYVGSSILS 60
 |||||
 Db 239 SDVYCEVCEFLVKEVTKLIDNNKTEKILDAFQKCSKLPKSLSECEQVVDYVGSSILS 298
 |||||

Qy 61 ILLREVSPELVCSMLHLCSG 80
 |||||
 Db 299 ILLREVSPELVCSMLHLCSG 318
 |||||

Wed Jan 18 11:58:43 2006

RESULT 2

SAP_HUMAN STANDARD; PRT; 524 AA.

ID Q67602; P07232; P15793; P78538; P78541; P78546; P78547; P78558;

AC Q67606; Q92739; Q92740; Q92741; Q92742;

OC Q1-APR-1988 (Rel. 07, Created)

DT 01-APR-1990 (Rel. 14, Last sequence update)

DT 13-SEP-2005 (Rel. 48, Last annotation update)

DE Proactivator polypeptide precursor [Contains: Saposin A (Protein A);

DE Saposin B-val; Saposin B (sphingolipid activator protein 1) (SAP-1)

DE (Cerebroside sulfate activator) (CSAct) (Dispersin) (Sulfatide/GM1

DE activator); Saposin C (Co-beta-glucosidase) (AI activator)

DE (Glucosylceramide activator) (Sphingolipid activator protein 2)

DE (SAP-2); Saposin D (Protein C) (Component C)].

GN Name=PSAP;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;

OC Homo.

OX NCBI_TaxID=9606;

RN [1]

RP NUCLEOTIDE SEQUENCE [MRNA].

RC TISSUE=Liver;

RX MEDLINE=90129043; PubMed=2515150;

RA Rorman E.G., Grabowski G.A.;

RT "Molecular cloning of a human co-beta-glucosidase cDNA: evidence that

RT four sphingolipid hydrolase activator proteins are encoded by single

RT genes in humans and rats.;"

RL J. Biochem. 105:152-154 (1989).

RN [2]

RP NUCLEOTIDE SEQUENCE [MRNA].

RX MEDLINE=89255151; PubMed=2498298;

RA Nakano T., Sandhoff K., Stuenkel J., Christomanou H., Suzuki K.;

RT "Structure of full-length cDNA coding for sulfatide activator, a Co-

RT beta-glucosidase and two other homologous proteins: two alternate

RT forms of the sulfatide activator.;"

RL J. Biochem. 105:152-154 (1989).

RN [3]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].

RX Ebert L., Schick M., Neubert P., Schatten R., Henze S., Korn B.;

RT "Cloning of human full open reading frames in Gateway(TM) system entry

RT vector (pDONR201).;"

RL Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.

RN [4]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM SAP-MU-0).

RC TISSUE=Brain, Eye, and Skin;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klauener R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Boak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gay L.J., Hulyk S.W.,

RA Richardson D.K., Worley K.C., Hale S., Garcia A.M., Gibbs R.A.,

RA Vallalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs S., Sanchez A.,

RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Bouffard G.G.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Dickinson M.C.,

RA Blakesley R.W., Touchman J.W., Green E.D., Myers R.M.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywicki M.I., Skalska U., Marra M.A.;

RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences.;"

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

RN [5]

RP NUCLEOTIDE SEQUENCE OF 14-524.

RX MEDLINE=88321660; PubMed=2842863;

RA O'Brien J.S., Kretz K.A., Dewji N., Wenger D.A., Esch F.,

RA Fluharty A.L.;

RT "Coding of two sphingolipid activator proteins (SAP-1 and SAP-2) by

RT same genetic locus.;"

RL Science 241:1098-1101 (1988).

RN [6]

RP NUCLEOTIDE SEQUENCE OF 14-524.

RX MEDLINE=92307663; PubMed=1612590;

RA Rorman E.G., Scheinker V., Grabowski G.A.;

RT "Structure and evolution of the human prosaposin chromosomal gene.;"

RL Genomics 13:312-318 (1992).

RN [7]

RP PROTEIN SEQUENCE OF 17-24; 165-172; 180-189 AND 298-302.

RX MEDLINE=93311991; PubMed=8323276; DOI=10.1006/abbi.1993.1328;

RA Hiraiwa M., O'Brien J.S., Kishimoto Y., Galdzicka M., Fluharty A.L.,

RA Gims E.I., Martin B.M.;

RT "Isolation, characterization, and proteolysis of human prosaposin, the

RT precursor of saposins (sphingolipid activator proteins).;"

RL Arch. Biochem. Biophys. 304:110-116 (1993).

RN [8]

RP PROTEIN SEQUENCE OF 17-26.

RC TISSUE=Milk;

RX MEDLINE=92068206; PubMed=1958198;

RA Kondoh K., Hinenio T., Sano A., Kakimoto Y.;

RT "Isolation and characterization of prosaposin from human milk.;"

RL Biochem. Biophys. Res. Commun. 181:286-292 (1991).

RN [9]

RP NUCLEOTIDE SEQUENCE OF 59-125 AND 304-513.

RX TISSUE=Brain; PubMed=2013321; DOI=10.1016/0014-5793(91)80308-P;

RA Holtschmidt H., Sandhoff K., Fuerst W., Kwon H.Y., Schnabel D.,

RA Suzuki K.;

RT "The organization of the gene for the human cerebroside sulfate

RT activator protein.;"

RL FEBS Lett. 280:267-270 (1991).

RN [10]

RP PARTIAL PROTEIN SEQUENCE OF 60-142.

RX MEDLINE=89240739; PubMed=2717620;

RA Morimoto S., Martin B.M., Yamamoto Y., Kretz K.A., O'Brien J.S.,

RA Kishimoto Y.;

RT "Saposin A: second cerebroside activator protein.;"

RL Proc. Natl. Acad. Sci. U.S.A. 86:3389-3393 (1989).

RN [11]

RP PROTEIN SEQUENCE OF 62-84 AND 410-431.

RX MEDLINE=93380576; PubMed=8370464; DOI=10.1016/0014-5793(93)80908-D;

RA Tyynela J., Palmer D.N., Baumann M., Haltia M.;

RT "Storage of saposins A and D in infantile neuronal ceroid-

RT lipofuscinosis.;"

RL FEBS Lett. 330:8-12 (1993).

RN [12]

RP NUCLEOTIDE SEQUENCE OF 164-524.

RX MEDLINE=88068647; PubMed=2825202;

RA Dewji N.N., Wenger D.A., O'Brien J.S.;

RT "Nucleotide sequence of cloned cDNA for human sphingolipid activator

RT protein 1 precursor.;"

RL Proc. Natl. Acad. Sci. U.S.A. 84:8652-8656 (1987).

RN [13]

RP NUCLEOTIDE SEQUENCE OF 195-263.

RX MEDLINE=86130593; PubMed=2868718;

RA Dewji N.N., Wenger D.A., Fujibayashi S., Donoviel M., Esch F.,

RA Hill F., O'Brien J.S.;

RT "Molecular cloning of the sphingolipid activator protein-1 (SAP-1),

RT the sulfatide sulfatase activator.;"

RL Biochem. Biophys. Res. Commun. 134:989-994 (1986).

RN [14]

RP PROTEIN SEQUENCE OF 195-274.

RX MEDLINE=89207118; PubMed=2324255;

RA Kleinschmidt T., Christomanou H., Braunitzer G.;

RT "Complete amino-acid sequence of the naturally occurring A2 activator

RT protein for enzymic sphingomyelin degradation: identity to the

RT sulfatide activator protein (SAP-1).;"

RL Biol. Chem. Hoppe-Seyler 369:1361-1365 (1988).

RN [15]

RP PROTEIN SEQUENCE OF 195-274.

RC TISSUE=Kidney;

RX MEDLINE=91006165; PubMed=2209618;

RA Furst W., Schubert J., Machleidt W., Meyer H.E., Sandhoff K.;
RT "The complete amino-acid sequences of human ganglioside GM2 activator
RL protein and cerebroside sulfate activator protein.";
RL Eur. J. Biochem. 192:709-714(1990).
RN [16]
RP PROTEIN SEQUENCE OF 311-390.
RX MEDLINE=88163077; PubMed=3442600;
RA Kleinschmidt T., Christomanou H., Braunitzer G.;
RT "Complete amino-acid sequence and carbohydrate content of the
RT naturally occurring glucosylceramide activator protein (A1 activator)
RT absent from a new human Gaucher disease variant.";
RL Biol. Chem. Hoppe-Seyler 368:1571-1578(1987).
RN [17]
RP PARTIAL PROTEIN SEQUENCE OF 405-484.
RX MEDLINE=89025876; PubMed=2845979;
RA Morimoto S., Martin B.M., Kishimoto Y., O'Brien J.S.;
RT "Saposin D: a sphingomyelinase activator.";
RL Biochem. Biophys. Res. Commun. 156:403-410(1988).
RN [18]
RP PROTEIN SEQUENCE OF 407-484.
RX MEDLINE=89000190; PubMed=3048308;
RA Furst W., Machleidt W., Sandhoff K.;
RT "The precursor of sulfatide activator protein is processed to three
RT different proteins.";
RL Biol. Chem. Hoppe-Seyler 369:317-328(1988).
RN [19]
RP PARTIAL PROTEIN SEQUENCE (SAPOSIN B), AND STRUCTURE OF CARBOHYDRATES.
RC TISSUE=Urine;
RX MEDLINE=20032116; PubMed=10562467; DOI=10.1006/mgme.1999.2900;
RA Fluharty A.L., Lombardo C., Louis A., Stevens R.L., Whitelegge J.P.,
RA Waring A.J., To T., Fluharty C.B., Faull K.F.;
RT "Preparation of the cerebroside sulfate activator (CSAct or saposin B)
RT from human urine.";
RL Mol. Genet. Metab. 68:391-403(1999).
RN [20]
RP DISULFIDE BONDS OF SAPOSINS B AND C, AND MASS SPECTROMETRY.
RX MEDLINE=95247730; PubMed=7730378; DOI=10.1074/jbc.270.17.9953;
RA Vaccaro A.M., Salviole R., Barca A., Tatti M., Claffoni F., Maras B.,
RA Siciliano R., Zappacosta P., Amoresano A., Pucci P.;
RT "Structural analysis of saposin C and B. Complete localization of
RT disulfide bridges.";
RL J. Biol. Chem. 270:9953-9960(1995).
RN [21]
RP STRUCTURE OF CARBOHYDRATE ON ASN-215.
RX MEDLINE=21110404; PubMed=11180632;
RA Faull K.F., Johnson J., Kim M.J., To T., Whitelegge J.P.,
RA Stevens R.L., Fluharty C.B., Fluharty A.L.;
RT "Structure of the asparagine-linked sugar chains of porcine kidney and
RT human urine cerebroside sulfate activator protein.";
RL J. Mass Spectrom. 35:1416-1424(2000).
RN [22]
RP SAPOSIN D DISULFIDE BONDS.
RX MEDLINE=99337688; PubMed=10406958;
RA Tatti M., Salviole R., Claffoni F., Pucci P., Andolfo A.,
RA Amoresano A., Vaccaro A.M.;
RT "Structural and membrane-binding properties of saposin D.";
RL Query Match 100.0%; Score 412; DB 1; Length 524;
Best Local Similarity 100.0%; Pred. NO. 2.6e-30;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SDVYCEVFLVKEVTKLIDNNKTEKILDAFKMCKSLPKSLSEECQEVVDYTGSSILS 60
DB 311 SDVYCEVFLVKEVTKLIDNNKTEKILDAFKMCKSLPKSLSEECQEVVDYTGSSILS 370
QY 61 ILLEEVSPVLCSMLHLCSSG 80
DB 371 ILLEEVSPVLCSMLHLCSSG 390
RESULT 3
Q53FJ5 HUMAN
ID Q53FJ5_HUMAN PRELIMINARY; PRT; 524 AA.

AC Q53FJ5;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Prosaposin (Variant Gaucher disease and variant metachromatic
DE leukodystrophy) variant (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Synovial membrane;
RA Maruyama K., Sugano S.;
RT "Oligo-capping: a simple method to replace the cap structure of
RT eucaryotic mRNAs with oligoribonucleotides.";
RL Gene 138:171-174(1994).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Synovial membrane;
RA Suzuki Y., Yoshitomo K., Maruyama K., Sugano S.;
RT "Construction and characterization of a full length-enriched and a 5'-
RT end-enriched cDNA library.";
RL Gene 200:149-156(1997).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Synovial membrane;
RA Tanaka A., Yokoyama S.;
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK23290; BAD97010.1; -; mRNA.
FT NON_TER 1
SQ SEQUENCE 524 AA; 58140 MW; 7034F0C71C2226BC CRC64;
Query Match 100.0%; Score 412; DB 2; Length 524;
Best Local Similarity 100.0%; Pred. NO. 2.6e-30;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SDVYCEVFLVKEVTKLIDNNKTEKILDAFKMCKSLPKSLSEECQEVVDYTGSSILS 60
DB 311 SDVYCEVFLVKEVTKLIDNNKTEKILDAFKMCKSLPKSLSEECQEVVDYTGSSILS 370
QY 61 ILLEEVSPVLCSMLHLCSSG 80
DB 371 ILLEEVSPVLCSMLHLCSSG 390
RESULT 4
Q5JQ36 HUMAN
ID Q5JQ36_HUMAN PRELIMINARY; PRT; 524 AA.
AC Q5JQ36;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Prosaposin (Variant Gaucher disease and variant metachromatic
DE leukodystrophy).
GN Names=PSAP; ORNames=RP11-472K8.1-001;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Synovial membrane;
RA Heath P.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Kalline N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
RA Koundinya M., Raphael J., Moreira D., Kelley T., Labaer J., Lin Y.,
RA Phelan M., Farmer A.;
RT "Cloning of human full-length CDSs in BD Creator(TM) System Donor

```

RT vector.";
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL731541; CAI40837.1; -; Genomic_DNA.
DR EMBL; BT006849; AAP35495.1; -; mRNA.
DR EMBL; AC073370; CAI40837.1; JOINED; Genomic_DNA.
DR GO; GO:0005764; C:lysosome; IEA.
DR GO; GO:0006629; P:lipid metabolism; IEA.
DR GO; GO:0006665; P:sphingolipid metabolism; IEA.
SQ SEQUENCE 524 AA; 58112 MW; 71977F7A8C9B1533 CRC64;

Query Match 100.0%; Score 412; DB 2; Length 524;
Best Local Similarity 100.0%; Pred. No. 2.6e-30;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDAFDMCKSLPKSLSECEQVVDVTYGSILS 60
Db 311 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDAFDMCKSLPKSLSECEQVVDVTYGSILS 370

Qy 61 ILLEEVSPVLVCSMLHLCSG 80
Db 371 ILLEEVSPVLVCSMLHLCSG 390

RESULT 5
ID Q5NVDS_PONPY PRELIMINARY; PRT; 527 AA.
AC Q5NVDS_PONPY
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Hypothetical protein DKFZp459F0110.
GN Name=DKFZp459F0110;
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC Tissue=Cortex;
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR926102; CAI29728.1; -; mRNA.
DR SMR; Q5NVDS; 194-275, 314-393.
DR GO; GO:0005764; C:lysosome; IEA.
DR GO; GO:0006629; P:lipid metabolism; IEA.
DR GO; GO:0006665; P:sphingolipid metabolism; IEA.
DR InterPro; IPR003119; Sapa.
DR InterPro; IPR007856; SApB.
DR InterPro; IPR008138; SApB_2.
DR InterPro; IPR008140; SApB_sub.
DR InterPro; IPR008373; Saposin.
DR InterPro; IPR008139; SaposinB.
DR Pfam; PF021199; Sapa; 2.
DR Pfam; PF05184; SApB_1; 4.
DR Pfam; PF03489; SApB_2; 4.
DR PRINTS; PR01797; SAPOSIN.
DR ProDom; PD001732; SApB_sub; 2.
DR SMART; SM00162; SAPA; 2.
KW Hypothetical protein.
SQ SEQUENCE 527 AA; 58469 MW; 293FBB746C29C4D0 CRC64;

Query Match 100.0%; Score 412; DB 2; Length 527;
Best Local Similarity 100.0%; Pred. No. 2.6e-30;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDAFDMCKSLPKSLSECEQVVDVTYGSILS 60
Db 314 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDAFDMCKSLPKSLSECEQVVDVTYGSILS 373

Qy 61 ILLEEVSPVLVCSMLHLCSG 80
Db 371 ILLEEVSPVLVCSMLHLCSG 390

vector.";
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL731541; CAI40837.1; -; Genomic_DNA.
DR EMBL; BT006849; AAP35495.1; -; mRNA.
DR EMBL; AC073370; CAI40837.1; JOINED; Genomic_DNA.
DR GO; GO:0005764; C:lysosome; IEA.
DR GO; GO:0006629; P:lipid metabolism; IEA.
DR GO; GO:0006665; P:sphingolipid metabolism; IEA.
SQ SEQUENCE 524 AA; 58112 MW; 71977F7A8C9B1533 CRC64;

Query Match 100.0%; Score 412; DB 2; Length 524;
Best Local Similarity 100.0%; Pred. No. 2.6e-30;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDAFDMCKSLPKSLSECEQVVDVTYGSILS 60
Db 311 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDAFDMCKSLPKSLSECEQVVDVTYGSILS 370

Qy 61 ILLEEVSPVLVCSMLHLCSG 80
Db 371 ILLEEVSPVLVCSMLHLCSG 390

RESULT 6
ID Q59EN5_HUMAN PRELIMINARY; PRT; 530 AA.
AC Q59EN5_HUMAN
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Prosaposin variant (Fragment).
GN Name=prosaposin variant;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC Tissue=Brain;
RA Totoki Y., Toyoda A., Takeda T., Sakaki Y., Tanaka A., Yokoyama S.,
RA Ohara O., Nagase T., Kikuno F.R.;
RT "None Title.";
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB209776; BAD93013.1; -; mRNA.
FT NON TER 1
SQ SEQUENCE 530 AA; 58727 MW; 6CA1F0159B182BC9 CRC64;

Query Match 100.0%; Score 412; DB 2; Length 530;
Best Local Similarity 100.0%; Pred. No. 2.6e-30;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDAFDMCKSLPKSLSECEQVVDVTYGSILS 60
Db 317 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDAFDMCKSLPKSLSECEQVVDVTYGSILS 376

Qy 61 ILLEEVSPVLVCSMLHLCSG 80
Db 377 ILLEEVSPVLVCSMLHLCSG 396

vector.";
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL731541; CAI40836.1; -; Genomic_DNA.
DR EMBL; AC073370; CAI40836.1; JOINED; Genomic_DNA.
DR SMR; Q5JQ37; 194-272, 311-390.
DR GO; GO:0005764; C:lysosome; IEA.
DR GO; GO:0006629; P:lipid metabolism; IEA.
DR GO; GO:0006665; P:sphingolipid metabolism; IEA.
DR InterPro; IPR003119; Sapa.
DR InterPro; IPR007856; SApB_1.
DR InterPro; IPR008138; SApB_2.
DR InterPro; IPR008140; SApB_sub.
DR InterPro; IPR008373; Saposin.
DR InterPro; IPR008139; SaposinB.
DR Pfam; PF021199; Sapa; 2.
DR Pfam; PF05184; SApB_1; 4.
DR Pfam; PF03489; SApB_2; 4.
DR PRINTS; PR01797; SAPOSIN.
DR ProDom; PD001732; SApB_sub; 2.
DR SMART; SM00162; SAPA; 2.
KW Hypothetical protein.
SQ SEQUENCE 527 AA; 58469 MW; 293FBB746C29C4D0 CRC64;

Query Match 100.0%; Score 412; DB 2; Length 527;
Best Local Similarity 100.0%; Pred. No. 2.6e-30;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDAFDMCKSLPKSLSECEQVVDVTYGSILS 60
Db 314 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDAFDMCKSLPKSLSECEQVVDVTYGSILS 373

Qy 61 ILLEEVSPVLVCSMLHLCSG 80
Db 371 ILLEEVSPVLVCSMLHLCSG 390

vector.";
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL731541; CAI40837.1; -; Genomic_DNA.
DR EMBL; BT006849; AAP35495.1; -; mRNA.
DR EMBL; AC073370; CAI40837.1; JOINED; Genomic_DNA.
DR GO; GO:0005764; C:lysosome; IEA.
DR GO; GO:0006629; P:lipid metabolism; IEA.
DR GO; GO:0006665; P:sphingolipid metabolism; IEA.
SQ SEQUENCE 524 AA; 58112 MW; 71977F7A8C9B1533 CRC64;

Query Match 100.0%; Score 412; DB 2; Length 524;
Best Local Similarity 100.0%; Pred. No. 2.6e-30;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDAFDMCKSLPKSLSECEQVVDVTYGSILS 60
Db 311 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDAFDMCKSLPKSLSECEQVVDVTYGSILS 370

Qy 61 ILLEEVSPVLVCSMLHLCSG 80
Db 371 ILLEEVSPVLVCSMLHLCSG 390

RESULT 7
ID Q5JQ37_HUMAN PRELIMINARY; PRT; 559 AA.
AC Q5JQ37_HUMAN
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Prosaposin (Variant Gaucher disease and variant metachromatic
DE leukodystrophy).
GN Name=PSAP; ORFNames=RP11-472K8.1-002;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC Heath P.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL731541; CAI40836.1; -; Genomic_DNA.
DR EMBL; AC073370; CAI40836.1; JOINED; Genomic_DNA.
DR SMR; Q5JQ37; 194-272, 311-390.
DR GO; GO:0005764; C:lysosome; IEA.
DR GO; GO:0006629; P:lipid metabolism; IEA.
DR GO; GO:0006665; P:sphingolipid metabolism; IEA.
DR InterPro; IPR003119; Sapa.
DR InterPro; IPR007856; SApB_1.
DR InterPro; IPR008138; SApB_2.
DR InterPro; IPR008140; SApB_sub.
DR InterPro; IPR008373; Saposin.
DR InterPro; IPR008139; SaposinB.

```

```
DR Pfam; PF02199; SapA; 2.
DR Pfam; PF05184; SapB 1; 4.
DR Pfam; PF03489; SapB 2; 4.
DR PRINTS; PR01797; SAPOSIN.
DR ProDom; PD001732; SapB sub; 2.
DR SMART; SM00162; SAPA; 2.
SQ SEQUENCE 559 AA; 61692 MW; 7C80741B6039AE38 CRC64;

Query Match 100.0%; Score 412; DB 2; Length 559;
Best Local Similarity 100.0%; Pred. No. 2.7e-30;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDMCKSLPKSLSEECQEVVDYTGSSILS 60
Db 311 SDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDMCKSLPKSLSEECQEVVDYTGSSILS 370
Qy 61 ILLEEVSPVLCSMLHLCSG 80
Db 371 ILLEEVSPVLCSMLHLCSG 390

RESULT 8
Q5RAU7_PONPY
ID Q5RAU7_PONPY PRELIMINARY; PRT; 526 AA.
AC Q5RAU7;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Hypothetical protein DKFp459J114.
GN Names=DKFp459J114;
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Pongo.
NCBI_TaxID=9600;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Cortex;
RG The German cDNA Consortium;
RA Bloeker H., Boecher M., Brandt P., Mewes H.W., Weil B., Amid C.,
RA Oranger A., Fobo G., Han M., Wiemann S.;
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR861144; CAH93219.1; -; mRNA.
DR SMR; Q5RAU7; 194-274, 313-392.
DR GO; GO:0005764; C:lysosome; IEA.
DR GO; GO:0006629; P:lipid metabolism; IEA.
DR GO; GO:0006665; P:sphingolipid metabolism; IEA.
DR InterPro; IPR003119; SapA.
DR InterPro; IPR007856; SapB 1.
DR InterPro; IPR008138; SapB 2.
DR InterPro; IPR008140; SapB sub.
DR InterPro; IPR008373; Saposin.
DR InterPro; IPR008139; SaposinB.
DR Pfam; PF02199; SapA; 2.
DR Pfam; PF05184; SapB 1; 4.
DR Pfam; PF03489; SapB 2; 4.
DR PRINTS; PR01797; SAPOSIN.
DR ProDom; PD001732; SapB sub; 2.
DR SMART; SM00162; SAPA; 2.
KW Hypothetical protein.
SQ SEQUENCE 526 AA; 58325 MW; CF3B146DDB6F5539 CRC64;

Query Match 98.3%; Score 405; DB 2; Length 526;
Best Local Similarity 98.8%; Pred. No. 1.2e-29;
Matches 79; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDMCKSLPKSLSEECQEVVDYTGSSILS 60
Db 313 SDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDMCKSLPKSLSEECQEVVDYTGSSILS 372
Qy 61 ILLEEVSPVLCSMLHLCSG 80
Db 373 ILLEEVSPVLCSMLHLCSG 392
```

RESULT 9

```
Q4R590_MACFA
ID Q4R590_MACFA PRELIMINARY; PRT; 497 AA.
AC Q4R590;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Brain cDNA, clone: QccE-13090, similar to human prosaposin (variant
DE Gaucher disease and variantmetachromatic leukodystrophy) (PSAP),
DE (Brain cDNA, clone: QccE-13989, similar to human prosaposin (variant
DE Gaucher disease and variantmetachromatic leukodystrophy)
DE (PSAP)).
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopitheidae; Cercopitheciae; Macaca.
NCBI_TaxID=9541;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC International consortium for macaque cDNA sequencing, analysis;
RT "DNA sequences of macaque genes expressed in brain or testis and its
RT evolutionary implications.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Osada N., Hirata M., Tanuma R., Kusuda J., Hida M., Suzuki Y.,
RA Sugano S., Gojobori T., Shen J.C.-K., Wu C.I., Hashimoto K.;
RT "Substitution rate and structural divergence of 5'UTR evolution:
RT Comparative analysis between human and cynomolgus monkey cDNAs.";
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB169654; BAE01735.1; -; mRNA.
DR EMBL; AB169527; BAE01609.1; -; mRNA.
SQ SEQUENCE 497 AA; 55306 MW; 4A1974F8DB883900 CRC64;

Query Match 96.4%; Score 397; DB 2; Length 497;
Best Local Similarity 96.2%; Pred. No. 6.3e-29;
Matches 77; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 SDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDMCKSLPKSLSEECQEVVDYTGSSILS 60
Db 314 SDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDMCKSLPKSLSEECQEVVDYTGSSILS 373
Qy 61 ILLEEVSPVLCSMLHLCSG 80
Db 374 ILLEEVSPVLCSMLHLCSG 393

RESULT 10
SAP_BOVIN
ID SAP_BOVIN STANDARD; PRT; 525 AA.
AC P26779; Q9NZG4;
DT 01-AUG-1992 (Rel. 23, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Proactivator polypeptide precursor [Contains: Saposin A (Protein A);
DE Saposin B (Sphingolipid activator protein 1) (SAP-1) (Cerebroside
DE sulfate activator) (CSact) (dispersin) (Sulfatide/GM1 activator);
DE Saposin C (Co-beta-glucosidase) (Al activator) (Glucosylceramidase
DE activator) (Sphingolipid activator protein 2) (SAP-2); Saposin D
DE (Protein C) (Component C)].
GN Names=PSAP;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE, AND VARIANTS.
RC TISSUE=Mammary gland;
RA Azuma N., Yoshida K.;
RT "RT-PCR cloning of bovine prosaposin.";
```

Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.

[2]

RL PROTEIN SEQUENCE OF 312-391.

RN TISSUE=Spleen;

RC MEDLINE=92207994; PubMed=1554743; DOI=10.1016/0167-4838(92)90426-E;

RC Sano A., Mizuno T., Kondoh K., Htano T., Ueno S.-I., Kakimoto Y.,

RA Morita N.;

RA "Saposin-C from bovine spleen; complete amino acid sequence and

RT relation between the structure and its biological activity.";

RL Biochim. Biophys. Acta 1120:75-80(1992).

RL -1- FUNCTION: The lysosomal degradation of sphingolipids takes place

CC by the sequential action of specific hydrolases. Some of these

CC enzymes require specific low-molecular mass, non-enzymic proteins:

CC the sphingolipids activator proteins (coproteins) (By similarity).

CC -1- FUNCTION: Saposin A and saposin C stimulate the hydrolysis of

CC galactosylceramide by beta-glucosylceramidase (EC 3.2.1.45) and

CC galactosylceramide by beta-galactosylceramidase (EC 3.2.1.46).

CC Saposin C apparently acts by combining with the enzyme and acidic

CC lipid to form an activated complex, rather than by solubilizing

CC the substrate.

CC -1- FUNCTION: Saposin B stimulates the hydrolysis of galacto-

CC cerebroside sulfate by arylsulfatase A (EC 3.1.6.8), GM1

CC gangliosides by beta-galactosidase (EC 3.2.1.23) and

CC globotriaosylceramide by alpha-galactosidase A (EC 3.2.1.22).

CC Saposin B forms a solubilizing complex with the substrates of the

CC sphingolipid hydrolases (By similarity).

CC -1- FUNCTION: Saposin D is a specific sphingomyelin phosphodiesterase

CC activator (EC 3.1.1.12) (By similarity).

CC -1- SUBUNIT: Saposin B is a homodimer (By similarity).

CC -1- SUBCELLULAR LOCATION: Lysosomal.

CC -1- PTM: This precursor is proteolytically processed to 4 small

CC peptides, which are similar to each other and are sphingolipid

CC hydrolase activator proteins (By similarity).

CC -1- SIMILARITY: Contains 2 saposin A-type domains.

CC -1- SIMILARITY: Contains 4 saposin B-type domains.

CC -----

CC This Swiss-Prot entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use as long as its content is in no way modified and this statement is not

CC removed.

CC -----

CC EMBL; AB036791; BAA95677.1; -; mRNA.

DR HSSP; Q92739; IM12.

DR SMR; P26779; 195-273, 312-390.

DR InterPro; IPR009007; Pept_Apartc_cat.

DR InterPro; IPR003119; SAPA.

DR InterPro; IPR007856; SAPB_1.

DR InterPro; IPR008138; SAPB_2.

DR InterPro; IPR008140; SAPB_sub.

DR InterPro; IPR008373; SaposinB.

DR InterPro; IPR008137; Surfactant_B.

DR Pfam; PF02199; SAPA; 2.

DR Pfam; PF05184; SAPB_1; 4.

DR Pfam; PF03489; SAPB_2; 4.

DR PRINTS; PR01797; SAPOSIN.

DR ProDom; PD001732; SapB_sub; 2.

DR ProDom; PD008002; Surfactant_B; 1.

DR SMART; SM00162; SAPA; 2.

DR SMART; SM00741; SAPB; 4.

DR PROSITE; PSS1110; SAP_A; 2.

DR PROSITE; PSS00015; SAP_B; 4.

DR Direct protein sequencing; Glycoprotein; Lipid metabolism; Lysosome;

KW Repeat; signal; sphingolipid metabolism.

KW Repeat; signal; sphingolipid metabolism.

FT SIGNAL 1 16

FT PROPEP 17 58

FT CHAIN 60 142 Saposin A.

FT PROPEP 144 195

FT CHAIN 196 275 Saposin B.

FT PROPEP 277 310

FT CHAIN 312 392 Saposin C.

FT


```
RA Jaillon O., Aury J.M., Brunet P., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anichoud V., Jubin C., Castellani V., Katinka M., Vacherie B.,
RA Bismont C., Skalli Z., Cattolico L., Poulain J., De Bernardinis V.,
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Winkler P., Lander E.S., Weissenbach J., Roest Crolius H.,
RA "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype."
RL Nature 431:946-957(2004).
RN [2]
RG NUCLEOTIDE SEQUENCE.
RL Genoscope, Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAAB01015006; CAG09494.1; -; Genomic_DNA.
FT NON TER 550 550
SQ SEQUENCE 550 AA; 60620 MW; 30FAEFA766357628 CRC64;

Query Match 50.2%; Score 207; DB 2; Length 550;
Best Local Similarity 39.0%; Pred. No. 5e-11;
Matches 30; Conservative 30; Mismatches 17; Indels 0; Gaps 0;

Qy 4 YCEVCEFLVKEVTKLIDNNKTEKILDAFDKMCCKLPKSLSECEQVVDVTGSSILSL 63
Db 339 FCAICEAVMKQLEAMLDKTTSEEVIAHVKVCSYLPSSMSQCKDLVEAYGEAIDLLV 398

Qy 64 BEVSPCLVCSMLHLCSG 80
Db 399 QQVDPKTVCTMLALCNG 415

RESULT 14
Q8UV24_BRARE PRELIMINARY; PRT; 520 AA.
AC Q8UV24;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DE Lysosomal cofactor/neutrotrophic factor prosaposin.
GN Name=psap;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Seo H.-C., Lie O., Fjose A., O'Brien J.S., Kishimoto Y.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF276996; AAL54381.1; -; mRNA.
DR HSPG; Q92739; I169.
DR Ensembl; ENSDARG00000013968; Danio rerio.
DR ZFIN; ZDB-GENE-020108-1; psap.
DR GO; GO:0005764; C:lysosome; IEA.
DR GO; GO:0006629; P:lipid metabolism; IEA.
DR GO; GO:0007585; P:respiratory gaseous exchange; IEA.
DR GO; GO:0006665; P:sphingolipid metabolism; IEA.
DR InterPro; IPR003119; Sapa.
DR InterPro; IPR007856; Sapa.
DR InterPro; IPR008138; Sapa.
DR InterPro; IPR008140; Sapa sub.
DR InterPro; IPR008373; Saposin.
DR InterPro; IPR008139; SaposinB.
DR InterPro; IPR008137; Surfactant_B.
PFam; PF02199; Sapa; 2.
```

```
DR Pfam; PF05184; SapB_1; 3.
DR Pfam; PF03489; SapB_2; 4.
DR PRINTS; PR01797; SAPOSIN.
DR ProDom; PD001732; SapB_sub; 2.
DR ProDom; PD008002; Surfactant_B; 1.
DR SMART; SM00162; SAPA; 2.
DR SMART; SM00741; SapB; 4.
SQ SEQUENCE 520 AA; 57431 MW; F9E620F84BA41CB5 CRC64;

Query Match 49.8%; Score 205; DB 2; Length 520;
Best Local Similarity 40.8%; Pred. No. 7.3e-11;
Matches 31; Conservative 26; Mismatches 19; Indels 0; Gaps 0;

Qy 5 CEVCEFLVKEVTKLIDNNKTEKILDAFDKMCCKLPKSLSECEQVVDVTGSSILSL 64
Db 312 CAICEAVMKIEIENIQDTSEAEIVQAVKVCNLTPLTQAQCKDLTIETYGQAILDLVQ 371

Qy 65 EVSPCLVCSMLHLCSG 80
Db 372 EADPKTVCSFLALCSG 387

RESULT 15
Q6P3G7_BRARE PRELIMINARY; PRT; 520 AA.
AC Q6P3G7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Prosaposin.
GN Name=psap;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Whole;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Colling P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Whole;
RA Strausberg R.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC063994; AAH63994.1; -; mRNA.
DR ZFIN; ZDB-GENE-020108-1; psap.
DR GO; GO:0005764; C:lysosome; IEA.
DR GO; GO:0006629; P:lipid metabolism; IEA.
DR GO; GO:0007585; P:respiratory gaseous exchange; IEA.
DR GO; GO:0006665; P:sphingolipid metabolism; IEA.
DR InterPro; IPR003119; Sapa.
DR InterPro; IPR007856; Sapa.
DR InterPro; IPR008137; Surfactant_B.
```


THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 13, 2006, 16:26:40 ; Search time 15.2318 Seconds
(without alignments)
2194.512 Million cell updates/sec

Title: US-10-801-517-2
Perfect score: 412
Sequence: 1 SDVYCEVCEFLVKEVTKLID.....ILLEEVSPVLVCSMLHLCSSG 80

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA_Main:*
1: /cgn2_6/prodata1/pubpaa/US07_PUBCOMB.pap:*
2: /cgn2_6/prodata1/pubpaa/US08_PUBCOMB.pap:*
3: /cgn2_6/prodata1/pubpaa/US09_PUBCOMB.pap:*
4: /cgn2_6/prodata1/pubpaa/US10A_PUBCOMB.pap:*
5: /cgn2_6/prodata1/pubpaa/US10B_PUBCOMB.pap:*
6: /cgn2_6/prodata1/pubpaa/US11_PUBCOMB.pap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	412	100.0	80	3	US-09-767-007A-3
2	412	100.0	80	3	US-09-753-126-3
3	412	100.0	80	4	US-10-330-697-3
4	412	100.0	80	4	US-10-746-442-24
5	412	100.0	80	5	US-10-801-517-2
6	412	100.0	80	6	US-11-036-867-24
7	412	100.0	210	5	US-10-473-127-1867
8	412	100.0	479	3	US-09-978-418-40
9	412	100.0	479	5	US-10-485-231-40
10	412	100.0	522	5	US-10-618-281-38
11	412	100.0	523	3	US-09-767-007A-2
12	412	100.0	523	5	US-10-473-127-1877
13	412	100.0	524	3	US-09-870-759-60
14	412	100.0	524	3	US-09-751-708A-60
15	412	100.0	524	4	US-10-267-502-386
16	412	100.0	524	4	US-10-408-765A-1207
17	412	100.0	524	4	US-10-746-442-23
18	412	100.0	524	4	US-10-428-817A-56
19	412	100.0	524	5	US-10-801-517-1
20	412	100.0	524	5	US-10-473-127-1865
21	412	100.0	524	5	US-10-473-127-1866
22	412	100.0	524	5	US-10-473-127-1868
23	412	100.0	524	5	US-10-473-127-1869
24	412	100.0	524	5	US-10-473-127-1871
25	412	100.0	524	5	US-10-473-127-1873
26	412	100.0	524	5	US-10-473-127-1874
27	412	100.0	524	5	US-10-473-127-1878

28	412	100.0	524	5	US-10-473-127-1879	Sequence 1879, Ap
29	412	100.0	524	5	US-10-473-127-1880	Sequence 1880, Ap
30	412	100.0	524	5	US-10-473-127-1881	Sequence 1881, Ap
31	412	100.0	524	5	US-10-473-127-1882	Sequence 1882, Ap
32	412	100.0	524	5	US-10-473-127-2041	Sequence 2041, Ap
33	412	100.0	524	6	US-11-036-867-23	Sequence 23, Appl
34	412	100.0	526	5	US-10-473-127-1875	Sequence 1875, Ap
35	412	100.0	527	3	US-09-870-759-61	Sequence 61, Appl
36	412	100.0	527	3	US-09-751-708A-61	Sequence 61, Appl
37	412	100.0	527	4	US-10-060-036-73	Sequence 73, Appl
38	412	100.0	527	4	US-10-428-817A-57	Sequence 57, Appl
39	412	100.0	527	5	US-10-473-127-1870	Sequence 1870, Ap
40	412	100.0	527	5	US-10-473-127-1872	Sequence 1872, Ap
41	412	100.0	527	5	US-10-473-127-1876	Sequence 1876, Ap
42	412	100.0	592	3	US-09-753-126-4	Sequence 4, Appl
43	412	100.0	592	4	US-10-330-697-4	Sequence 4, Appl
44	355	86.2	227	4	US-10-452-858C-11	Sequence 11, Appl
45	257	62.4	209	4	US-10-043-487-340	Sequence 340, App

ALIGNMENTS

RESULT 1
US-09-767-007A-3
; Sequence 3, Application US/09767007A
; Patent No. US2002007275A1
; GENERAL INFORMATION:
; APPLICANT: John S. O'Brien
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS COMPRISING
; TITLE OF INVENTION: SAPOGIN C AND NEUROTROPIC PEPTIDES DERIVED THEREFROM
; FILE REFERENCE: MYELOS 2DC1C1
; CURRENT APPLICATION NUMBER: US/09/767,007A
; PRIORITY FILING DATE: 2001-01-22
; PRIOR APPLICATION NUMBER: 08/958,970
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial peptide
US-09-767-007A-3

Query Match 100.0%; Score 412; DB 3; Length 80;
Best Local Similarity 100.0%; Pred. No. 8.4e-37;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDKMKCKLPKLSLSECCQEVVDYTGSSILS 60
Db 1 SDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDKMKCKLPKLSLSECCQEVVDYTGSSILS 60
QY 61 ILLEEVSPVLVCSMLHLCSSG 80
Db 61 ILLEEVSPVLVCSMLHLCSSG 80

RESULT 2
US-09-753-126-3
; Sequence 3, Application US/09753126
; Patent No. US20020127219A1
; GENERAL INFORMATION:
; APPLICANT: OKKELS, JENS SIGURD
; APPLICANT: JENSEN, ANNE DAM
; APPLICANT: HALKIER, TORBEN
; APPLICANT: JENSEN, RIKKE BOLDING
; TITLE OF INVENTION: IMPROVED LYSOSOMAL ENZYMES AND LYSOSOMAL ENZYME
; TITLE OF INVENTION: ACTIVATORS
; FILE REFERENCE: 31-000600US
; CURRENT APPLICATION NUMBER: US/09/753,126

Wed Jan 18 11:58:42 2006

```

; CURRENT FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: PA 1999 01891
; PRIOR FILING DATE: 1999-12-30
; PRIOR APPLICATION NUMBER: 60/174,652
; PRIOR FILING DATE: 2000-01-06
; PRIOR APPLICATION NUMBER: PA 200 00865
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: 60/210,984
; PRIOR FILING DATE: 2000-06-12
; PRIOR APPLICATION NUMBER: 60/211,124
; PRIOR FILING DATE: 2000-06-12
; PRIOR APPLICATION NUMBER: PA 2000 01027
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 60/217,497
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/217,497
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-753-126-3

```

```

Query Match      100.0%; Score 412; DB 3; Length 80;
Best Local Similarity 100.0%; Pred. No. 8.4e-37;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDKMKSLPKSLSECCQEVVDYTGSSILS 60
    |||||||
DB 1 SDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDKMKSLPKSLSECCQEVVDYTGSSILS 60

QY 61 ILLEEVSPELVCSMLHLCSSG 80
    |||||||
DB 61 ILLEEVSPELVCSMLHLCSSG 80

```

```

RESULT 3
US-10-330-697-3
; Sequence 3, Application US/10330697
; Publication No. US20040009165A1
; GENERAL INFORMATION:
; APPLICANT: JENSEN, ANNE DAM
; APPLICANT: JENSEN, TORBEN
; APPLICANT: HALKIER, TORBEN
; APPLICANT: JENSEN, RIKKE BOLDING
; TITLE OF INVENTION: IMPROVED LYSOSOMAL ENZYMES AND LYSOSOMAL ENZYME
; TITLE OF INVENTION: ACTIVATORS
; FILE REFERENCE: 31-000600US
; CURRENT APPLICATION NUMBER: US/10/330,697
; CURRENT FILING DATE: 2002-12-27
; PRIOR APPLICATION NUMBER: US/09/753,126
; PRIOR FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: PA 1999 01891
; PRIOR FILING DATE: 1999-12-30
; PRIOR APPLICATION NUMBER: 60/174,652
; PRIOR FILING DATE: 2000-01-06
; PRIOR APPLICATION NUMBER: PA 200 00865
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: 60/210,984
; PRIOR FILING DATE: 2000-06-12
; PRIOR APPLICATION NUMBER: 60/211,124
; PRIOR FILING DATE: 2000-06-12
; PRIOR APPLICATION NUMBER: PA 2000 01027
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 60/217,497
; PRIOR FILING DATE: 2000-07-11
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-330-697-3

```

```

Query Match      100.0%; Score 412; DB 4; Length 80;
Best Local Similarity 100.0%; Pred. No. 8.4e-37;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDKMKSLPKSLSECCQEVVDYTGSSILS 60
    |||||||
DB 1 SDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDKMKSLPKSLSECCQEVVDYTGSSILS 60

QY 61 ILLEEVSPELVCSMLHLCSSG 80
    |||||||
DB 61 ILLEEVSPELVCSMLHLCSSG 80

```

```

RESULT 4
US-10-746-442-24
; Sequence 24, Application US/10746442
; Publication No. US20040121958A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, John S.
; TITLE OF INVENTION: METHODS FOR ALLEVIATING NEUROPATHIC PAIN
; FILE REFERENCE: 07256/024001
; CURRENT APPLICATION NUMBER: US/10/746,442
; CURRENT FILING DATE: 2003-12-24
; PRIOR APPLICATION NUMBER: APPLICATION NUMBER: US/08/928,074
; PRIOR FILING DATE: FILING DATE: 1997-09-11
; PRIOR APPLICATION NUMBER: APPLICATION NUMBER: 08/611,307
; PRIOR FILING DATE: FILING DATE: 1996-03-05
; PRIOR APPLICATION NUMBER: APPLICATION NUMBER: PCT/US97/04143
; PRIOR FILING DATE: FILING DATE: 1996-03-05
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Artificial
; OTHER INFORMATION: Peptide Sequence
; US-10-746-442-24

```

```

Query Match      100.0%; Score 412; DB 4; Length 80;
Best Local Similarity 100.0%; Pred. No. 8.4e-37;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDKMKSLPKSLSECCQEVVDYTGSSILS 60
    |||||||
DB 1 SDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDKMKSLPKSLSECCQEVVDYTGSSILS 60

QY 61 ILLEEVSPELVCSMLHLCSSG 80
    |||||||
DB 61 ILLEEVSPELVCSMLHLCSSG 80

```

```

RESULT 5
US-10-801-517-2
; Sequence 2, Application US/10801517
; Publication No. US20040229799A1
; GENERAL INFORMATION:
; APPLICANT: Qi, Xiaoyang
; APPLICANT: Children's Hospital Medical Center
; TITLE OF INVENTION: Saposin C-DOPS A Novel Anti-Tumor Agent
; FILE REFERENCE: CHM08/GN003
; CURRENT APPLICATION NUMBER: US/10/801,517
; CURRENT FILING DATE: 2004-03-16
; PRIOR APPLICATION NUMBER: 60/466,166
; PRIOR FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Homo sapiens

```

US-10-801-517-2

Query Match 100.0%; Score 412; DB 5; Length 80;
Best Local Similarity 100.0%; Pred. No. 8.4e-37; Indels 0; Gaps 0;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDKMCSEKLPKSLSEECQEVVDYTGSSILS 60
DB 1 SDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDKMCSEKLPKSLSEECQEVVDYTGSSILS 60
QY 61 ILLEEVSPELVCSMLHLCSSG 80
DB 61 ILLEEVSPELVCSMLHLCSSG 80

RESULT 6

US-11-036-867-24
; Sequence 24, Application US/11036867
; Publication No. US20050164948A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, John S.
; TITLE OF INVENTION: METHODS FOR ALLEVIATING NEUROPATHIC PAIN
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: US
; ZIP: 92037

COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/036,867
; FILING DATE: 14-Jan-2005
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/928,074
; FILING DATE: 11-SEP-1997
; APPLICATION NUMBER: 08/611,307
; FILING DATE: 05-MAR-1996
; APPLICATION NUMBER: PCT/US97/04143
; FILING DATE: 05-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Halle, Ph.D., Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07256/024001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 80 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-11-036-867-24

Query Match 100.0%; Score 412; DB 6; Length 80;
Best Local Similarity 100.0%; Pred. No. 8.4e-37; Indels 0; Gaps 0;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDKMCSEKLPKSLSEECQEVVDYTGSSILS 60
DB 1 SDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDKMCSEKLPKSLSEECQEVVDYTGSSILS 60
QY 61 ILLEEVSPELVCSMLHLCSSG 80
DB 61 ILLEEVSPELVCSMLHLCSSG 80

RESULT 7

US-10-473-127-1867
; Sequence 1867, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1867
; LENGTH: 210
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1867

Query Match 100.0%; Score 412; DB 5; Length 210;
Best Local Similarity 100.0%; Pred. No. 2.8e-36; Indels 0; Gaps 0;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDKMCSEKLPKSLSEECQEVVDYTGSSILS 60
DB 8 SDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDKMCSEKLPKSLSEECQEVVDYTGSSILS 67
QY 61 ILLEEVSPELVCSMLHLCSSG 80
DB 68 ILLEEVSPELVCSMLHLCSSG 87

RESULT 8

US-09-978-418-40
; Sequence 40, Application US/09978418
; Publication No. US20030118997A1
; GENERAL INFORMATION:
; APPLICANT: Bejanin, Stephan
; APPLICANT: Tanaka, Hiroaki
; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
; FILE REFERENCE: 142.USS.REG
; CURRENT APPLICATION NUMBER: US/09/978,418
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/311,305
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/314,734
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/318,204
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: 60/326,470
; PRIOR FILING DATE: 2001-10-01
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: JPatent
; SEQ ID NO 40
; LENGTH: 479
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-978-418-40
Query Match 100.0%; Score 412; DB 3; Length 479;
Best Local Similarity 100.0%; Pred. No. 7.8e-36;

Wed Jan 18 11:58:42 2006

Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDKMCCKLPKSLSECCQEVVDYTGSSILS 60
 Db 314 SDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDKMCCKLPKSLSECCQEVVDYTGSSILS 373
 QY 61 ILLEEVSPELVCSMLHLCSSG 80
 Db 374 ILLEEVSPELVCSMLHLCSSG 393

RESULT 9
 US-10-485-231-40
 ; Sequence 40, Application US/10485231
 ; Publication No. US2005011917A1
 ; GENERAL INFORMATION:
 ; APPLICANT: GENSET
 ; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
 ; FILE REFERENCE: 142.WO1
 ; CURRENT APPLICATION NUMBER: US/10/485,231
 ; CURRENT FILING DATE: 2004-01-29
 ; PRIOR APPLICATION NUMBER: 60/311,305
 ; PRIOR FILING DATE: 2001-08-10
 ; PRIOR APPLICATION NUMBER: 60/314,734
 ; PRIOR FILING DATE: 2001-08-24
 ; PRIOR APPLICATION NUMBER: 60/318,204
 ; PRIOR FILING DATE: 2001-09-07
 ; PRIOR APPLICATION NUMBER: 60/326,470
 ; PRIOR FILING DATE: 2001-10-01
 ; NUMBER OF SEQ ID NOS: 52
 ; SOFTWARE: Jpatent
 ; SEQ ID NO 40
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-485-231-40

Query Match 100.0%; Score 412; DB 5; Length 479;
 Best Local Similarity 100.0%; Pred. No. 7.8e-36; Indels 0; Gaps 0;
 Matches 80; Conservative 0; Mismatches 0;
 QY 1 SDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDKMCCKLPKSLSECCQEVVDYTGSSILS 60
 Db 314 SDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDKMCCKLPKSLSECCQEVVDYTGSSILS 373
 QY 61 ILLEEVSPELVCSMLHLCSSG 80
 Db 374 ILLEEVSPELVCSMLHLCSSG 393

RESULT 10
 US-10-618-281-38
 ; Sequence 38, Application US/10618281
 ; Publication No. US20040219609A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Day, Anthony G.
 ; APPLICANT: Estell, David A.
 ; APPLICANT: Lyons, Eric H.
 ; APPLICANT: Yao, Jian
 ; TITLE OF INVENTION: Methods for Modulating Proteases Not
 ; TITLE OF INVENTION: Previously Known as Proteases
 ; FILE REFERENCE: GC773-2
 ; CURRENT APPLICATION NUMBER: US/10/618,281
 ; CURRENT FILING DATE: 2003-07-11
 ; PRIOR APPLICATION NUMBER: US 60/395,325
 ; PRIOR FILING DATE: 2002-07-12
 ; NUMBER OF SEQ ID NOS: 92
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 38
 ; LENGTH: 522
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-618-281-38

Query Match 100.0%; Score 412; DB 5; Length 522;
 Best Local Similarity 100.0%; Pred. No. 8.6e-36; Indels 0; Gaps 0;
 Matches 80; Conservative 0; Mismatches 0;
 QY 1 SDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDKMCCKLPKSLSECCQEVVDYTGSSILS 60
 Db 309 SDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDKMCCKLPKSLSECCQEVVDYTGSSILS 368
 QY 61 ILLEEVSPELVCSMLHLCSSG 80
 Db 369 ILLEEVSPELVCSMLHLCSSG 388

RESULT 11
 US-09-767-007A-2
 ; Sequence 2, Application US/09767007A
 ; Patent No. US2002007725A1
 ; GENERAL INFORMATION:
 ; APPLICANT: John S. O'Brien
 ; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS COMPRISING
 ; FILE REFERENCE: MYELOS.2DC1C1
 ; CURRENT APPLICATION NUMBER: US/09/767,007A
 ; CURRENT FILING DATE: 2001-01-22
 ; PRIOR APPLICATION NUMBER: 08/958,970
 ; PRIOR FILING DATE: 1997-10-28
 ; NUMBER OF SEQ ID NOS: 11
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 2
 ; LENGTH: 523
 ; TYPE: PRT
 ; ORGANISM: homo sapiens
 US-09-767-007A-2

Query Match 100.0%; Score 412; DB 3; Length 523;
 Best Local Similarity 100.0%; Pred. No. 8.7e-36; Indels 0; Gaps 0;
 Matches 80; Conservative 0; Mismatches 0;
 QY 1 SDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDKMCCKLPKSLSECCQEVVDYTGSSILS 60
 Db 310 SDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDKMCCKLPKSLSECCQEVVDYTGSSILS 369
 QY 61 ILLEEVSPELVCSMLHLCSSG 80
 Db 370 ILLEEVSPELVCSMLHLCSSG 389

RESULT 12
 US-10-473-127-1877
 ; Sequence 1877, Application US/10473127
 ; Publication No. US20040236091A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Zycos Inc.
 ; TITLE OF INVENTION: TRANSLATIONAL PROFILING
 ; FILE REFERENCE: 08191-026WO1
 ; CURRENT APPLICATION NUMBER: US/10/473,127
 ; CURRENT FILING DATE: 2003-09-26
 ; PRIOR APPLICATION NUMBER: 60/279,495
 ; PRIOR FILING DATE: 2001-03-28
 ; PRIOR APPLICATION NUMBER: 60/292,544
 ; PRIOR FILING DATE: 2001-05-21
 ; PRIOR APPLICATION NUMBER: 60/310,801
 ; PRIOR FILING DATE: 2001-08-08
 ; PRIOR APPLICATION NUMBER: 60/326,370
 ; PRIOR FILING DATE: 2001-10-01
 ; PRIOR APPLICATION NUMBER: 60/336,780
 ; PRIOR FILING DATE: 2001-12-04
 ; PRIOR APPLICATION NUMBER: 60/358,985
 ; PRIOR FILING DATE: 2002-02-20
 ; NUMBER OF SEQ ID NOS: 2041
 ; SOFTWARE: FastSeq for Windows Version 4.0


```
; SEQ ID NO 1877
; LENGTH: 523
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1877

Query Match      100.0%; Score 412; DB 5; Length 523;
Best Local Similarity 100.0%; Pred. No. 8.7e-36;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SDVYCEVCFVLKVEVTKLIDNNKTEKEILDAPDKMCKLPKSLSEECQEVVDYTGSSILS 60
Db 310 SDVYCEVCFVLKVEVTKLIDNNKTEKEILDAPDKMCKLPKSLSEECQEVVDYTGSSILS 369

QY 61 ILLEEVSPVLCSMLHLCSSG 80
Db 370 ILLEEVSPVLCSMLHLCSSG 389

RESULT 13
US-09-870-759-60
; Sequence 60, Application US/09870759
; Patent No. US20020177551A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 870759
; CURRENT APPLICATION NUMBER: US/09/870,759
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/208,128
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 60
; LENGTH: 524
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-870-759-60

Query Match      100.0%; Score 412; DB 3; Length 524;
Best Local Similarity 100.0%; Pred. No. 8.7e-36;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SDVYCEVCFVLKVEVTKLIDNNKTEKEILDAPDKMCKLPKSLSEECQEVVDYTGSSILS 60
Db 311 SDVYCEVCFVLKVEVTKLIDNNKTEKEILDAPDKMCKLPKSLSEECQEVVDYTGSSILS 370

QY 61 ILLEEVSPVLCSMLHLCSSG 80
Db 371 ILLEEVSPVLCSMLHLCSSG 390

RESULT 14
US-09-751-708A-60
; Sequence 60, Application US/09751708A
; Publication No. US20030157113A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 751708
; CURRENT APPLICATION NUMBER: US/09/751,708A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/173,371
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 60
; LENGTH: 524
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-751-708A-60

Query Match      100.0%; Score 412; DB 3; Length 524;
```

```
Best Local Similarity 100.0%; Pred. No. 8.7e-36;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SDVYCEVCFVLKVEVTKLIDNNKTEKEILDAPDKMCKLPKSLSEECQEVVDYTGSSILS 60
Db 311 SDVYCEVCFVLKVEVTKLIDNNKTEKEILDAPDKMCKLPKSLSEECQEVVDYTGSSILS 370

QY 61 ILLEEVSPVLCSMLHLCSSG 80
Db 371 ILLEEVSPVLCSMLHLCSSG 390

RESULT 15
US-10-267-502-386
; Sequence 386, Application US/10267502
; Publication No. US20040071700A1
; GENERAL INFORMATION:
; APPLICANT: Kim, Jaeseob
; APPLICANT: Galant, Ron
; TITLE OF INVENTION: Obesity Linked Genes
; FILE REFERENCE: LSD-07416
; CURRENT APPLICATION NUMBER: US/10/267,502
; CURRENT FILING DATE: 2003-01-27
; NUMBER OF SEQ ID NOS: 439
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 386
; LENGTH: 524
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-267-502-386

Query Match      100.0%; Score 412; DB 4; Length 524;
Best Local Similarity 100.0%; Pred. No. 8.7e-36;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SDVYCEVCFVLKVEVTKLIDNNKTEKEILDAPDKMCKLPKSLSEECQEVVDYTGSSILS 60
Db 311 SDVYCEVCFVLKVEVTKLIDNNKTEKEILDAPDKMCKLPKSLSEECQEVVDYTGSSILS 370

QY 61 ILLEEVSPVLCSMLHLCSSG 80
Db 371 ILLEEVSPVLCSMLHLCSSG 390

Search completed: January 13, 2006, 16:38:41
Job time : 15.2318 secs
```

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 13, 2006, 16:30:30 ; Search time 1.5894 Seconds
(without alignments)
475.862 Million cell updates/sec

Title: US-10-801-517-2

Perfect score: 412

Sequence: 1 SDVCEVCEFLVKEVTKLID.....ILLEVSPVLCSMLHLCSSG 80

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 67062 seqs, 9454214 residues

Total number of hits satisfying chosen parameters: 67062

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA_New.*
1: /cgn2_6/prodata/2/pubpaa/US08_NEW_PUB.pep.*
2: /cgn2_6/prodata/2/pubpaa/US06_NEW_PUB.pep.*
3: /cgn2_6/prodata/2/pubpaa/US07_NEW_PUB.pep.*
4: /cgn2_6/prodata/2/pubpaa/PCT_NEW_PUB.pep.*
5: /cgn2_6/prodata/2/pubpaa/US09_NEW_PUB.pep.*
6: /cgn2_6/prodata/2/pubpaa/US10_NEW_PUB.pep.*
7: /cgn2_6/prodata/2/pubpaa/US11_NEW_PUB.pep.*
8: /cgn2_6/prodata/2/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	412	100.0	524	6	US-10-821-234-1631
2	70.5	17.1	129	7	US-11-078-469-20
3	70.5	17.1	172	7	US-11-078-469-22
4	70	17.0	1786	7	US-11-196-400-3
5	67.5	16.4	145	7	US-11-078-469-21
6	65	15.8	989	6	US-10-821-234-975
7	64	15.5	476	6	US-10-878-556A-158
8	61.5	14.9	115	6	US-10-467-657-5296
9	61	14.8	292	7	US-11-194-246-316
10	60	14.6	2036	7	US-11-124-368A-276
11	60	14.6	2036	7	US-11-124-368A-280
12	60	14.6	2036	7	US-11-124-368A-281
13	59.5	14.4	3002	6	US-10-821-234-916
14	59	14.3	197	5	US-09-940-308-3
15	59	14.3	389	5	US-09-940-308-6
16	59	14.3	590	5	US-09-940-308-2
17	57.5	14.0	738	7	US-11-078-469-19
18	57.5	14.0	1138	6	US-10-509-422-4
19	57.5	14.0	5935	6	US-10-995-561-776
20	57	13.8	1087	7	US-11-102-978-2
21	57	13.8	1400	6	US-10-821-234-1045
22	56.5	13.7	122	6	US-10-793-626-564
23	56.5	13.7	248	6	US-10-793-626-464
24	55.5	13.5	372	6	US-10-844-035-1
25	55.5	13.5	373	6	US-10-995-561-948

26 55.5 13.5 375 6 US-10-995-561-946 Sequence 946, App
27 55.5 13.5 385 6 US-10-995-561-945 Sequence 945, App
28 55.5 13.5 385 6 US-10-995-561-949 Sequence 949, App
29 55.5 13.5 453 6 US-10-466-794A-5 Sequence 5, Appli
30 55.5 13.5 523 6 US-10-467-657-5392 Sequence 5392, Ap
31 55.5 13.5 854 6 US-10-511-657-4 Sequence 4, Appli
32 55.5 13.5 979 6 US-10-636-320-6 Sequence 6, Appli
33 55 13.3 369 6 US-10-763-712A-45 Sequence 45, Appli
34 55 13.3 369 6 US-10-763-712A-106 Sequence 106, App
35 55 13.3 431 7 US-11-074-176-132 Sequence 132, App
36 55 13.3 964 7 US-11-089-551A-30 Sequence 30, Appl
37 54.5 13.2 366 6 US-10-821-234-1447 Sequence 1447, Ap
38 54 13.1 457 6 US-10-467-657-2172 Sequence 2172, Ap
39 54 13.1 540 6 US-10-821-234-1456 Sequence 1456, Ap
40 54 13.1 687 7 US-11-074-176-260 Sequence 260, App
41 53.5 13.0 141 6 US-10-527-500-81 Sequence 81, Appl
42 53.5 13.0 179 6 US-10-467-657-2566 Sequence 2566, Ap
43 53.5 13.0 540 7 US-11-196-400-22 Sequence 22, Appl
44 53.5 13.0 629 6 US-10-821-234-1528 Sequence 1528, Ap
45 53.5 13.0 880 6 US-10-513-786-5 Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-10-821-234-1631
; Sequence 1631, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; PRIOR FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt SEQ_genes Version 1.0
; SEQ ID NO 1631
; LENGTH: 524
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1631

Query Match 100.0%; Score 412; DB 6; Length 524;
Best Local Similarity 100.0%; Pred. No. 7.7e-38;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SDVCEVCEFLVKEVTKLIDNNKTEKELDAPDKMCKLPKSLSECCQEVWDTYSSILS 60
Db 311 SDVCEVCEFLVKEVTKLIDNNKTEKELDAPDKMCKLPKSLSECCQEVWDTYSSILS 370
QY 61 ILLEVSPELVCSMLHLCSSG 80
Db 371 ILLEVSPELVCSMLHLCSSG 390

RESULT 2
US-11-078-469-20
; Sequence 20, Application US/11078469
; Publication No. US20050282755A1
; GENERAL INFORMATION:
; APPLICANT: HART, SCOTT A.
; APPLICANT: ZEH, KARIN
; APPLICANT: MACHLEIDT, THOMAS
; APPLICANT: STOLOV, DAVID
; APPLICANT: CONGER, DEB
; TITLE OF INVENTION: COMPOSITIONS HAVING ANTIMICROBIAL ACTIVITY AND USES
; TITLE OF INVENTION: THEREOF

us-10-801-517-2.rapbn

Wed Jan 18 11:58:42 2006

```

; APPLICANT: DRUILHE, PIERRE
; APPLICANT: DAUBERSIES, PIERRE
; TITLE OF INVENTION: MALARIAL PRE-ERYTHROCYTIC STAGE POLYPEPTIDE MOLECULES
; FILE REFERENCE: 200773USODIV
; CURRENT APPLICATION NUMBER: US/11/196,400
; CURRENT FILING DATE: 2005-08-04
; PRIOR APPLICATION NUMBER: US/09/742,096
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 08/973,462
; PRIOR FILING DATE: 1998-02-06
; PRIOR APPLICATION NUMBER: PCT/FR96/00894
; PRIOR FILING DATE: 1996-06-12
; PRIOR APPLICATION NUMBER: FR 95/07007
; PRIOR FILING DATE: 1995-06-13
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 3
; LENGTH: 1786
; TYPE: PRT
; ORGANISM: P. falciparum
; US-11-196-400-3

Query Match 17.1%; Score 70.5; DB 7; Length 129;
Best Local Similarity 21.1%; Pred. No. 0.31;
Matches 15; Conservative 21; Mismatches 34; Indels 1; Gaps 1;

Qy 8 CEFLVKEVTKLIDNNKTEKILDAFDKMSKLPKSLSEECQEVVDYTGSSILSILLEVS 67
Db 53 CLTIVQKLKQWVD-KPTQRSVSNAAATVCGTGRSRWDCVCFNFRYQSRVIOQLVAGET 111
Qy 68 PELVCSMLHLC 78
Db 112 AQICEDRLRC 122

RESULT 3
US-11-078-469-22
; Sequence 22, Application US/11/078469
; Publication No. US20050282755A1
; GENERAL INFORMATION:
; APPLICANT: HART, SCOTT A.
; APPLICANT: ZEH, KARIN
; APPLICANT: MACHLEIDT, THOMAS
; APPLICANT: STOLOV, DAVID
; APPLICANT: CONGER, DEE
; TITLE OF INVENTION: COMPOSITIONS HAVING ANTIMICROBIAL ACTIVITY AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ANS-2001-UT
; CURRENT APPLICATION NUMBER: US/11/078,469
; CURRENT FILING DATE: 2005-03-11
; PRIOR APPLICATION NUMBER: 60/554,526
; PRIOR FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: 60/618,948
; PRIOR FILING DATE: 2004-10-15
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: Patentin Ver. 3.3
; SEQ ID NO 22
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-078-469-22

Query Match 17.1%; Score 70.5; DB 7; Length 172;
Best Local Similarity 21.1%; Pred. No. 0.43;
Matches 15; Conservative 21; Mismatches 34; Indels 1; Gaps 1;

Qy 8 CEFLVKEVTKLIDNNKTEKILDAFDKMSKLPKSLSEECQEVVDYTGSSILSILLEVS 67
Db 96 CLTIVQKLKQWVD-KPTQRSVSNAAATVCGTGRSRWDCVCFNFRYQSRVIOQLVAGET 154
Qy 68 PELVCSMLHLC 78
Db 155 AQICEDRLRC 165

RESULT 4
US-11-196-400-3
; Sequence 3, Application US/11/196400
; Publication No. US20050287166A1
; GENERAL INFORMATION:

```

```
; Sequence 975, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: Pf_SEQ_genes Version 1.0
; SEQ ID NO 975
; LENGTH: 989
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-975

Query Match          15.8%; Score 65; DB 6; Length 989;
Best Local Similarity 26.0%; Pred. No. 14;
Matches 20; Conservative 16; Mismatches 31; Indels 10; Gaps 2;

QY 4 YCEVCEPLVKVTKLIDN-NKTEKEILDADFCKMCKSLPKSLSECCQVVDYTGSSI-----58
DB 592 YCSVIENNKEKAPLFKYQAEIIMKLDITLKSQMTQASDEADMKAMRMIDELN 651

QY 59 -----LSILIEVSPDL 70
DB 652 KQVSELSQLYKEAQEL 668

RESULT 7
US-10-878-556A-158
; Sequence 158, Application US/10878556A
; Publication No. US20050266399A1
; GENERAL INFORMATION:
; APPLICANT: Hoffmann La-Roche Inc.
; TITLE OF INVENTION: HCV regulated protein expression
; FILE REFERENCE: 21762
; CURRENT APPLICATION NUMBER: US/10/878,556A
; CURRENT FILING DATE: 2004-06-28
; NUMBER OF SEQ ID NOS: 199
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 158
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: humangp/chr19-q96g16
; DATABASE ENTRY DATE: 2003-04-22
US-10-878-556A-158

Query Match          15.5%; Score 64; DB 6; Length 476;
Best Local Similarity 31.7%; Pred. No. 7.6;
Matches 19; Conservative 10; Mismatches 19; Indels 12; Gaps 2;

QY 18 LIDNNKTEKETLDA-----FDKMCCKLPKSL--SECCQVVDYTGSSILSILIEE 65
DB 244 IVQENKGLKVLIEATKAFLDNPGILSELCTLSRLAETNEFCQEVVDLGLSILVSLAD 303

RESULT 8
US-10-467-657-5296
; Sequence 5296, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
```

```
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 5296
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-5296

Query Match          14.9%; Score 61.5; DB 6; Length 115;
Best Local Similarity 20.5%; Pred. No. 2.6;
Matches 17; Conservative 21; Mismatches 24; Indels 21; Gaps 3;

QY 12 VKEVTKLIDNNKTEKEILDADFCKMCKSLPKSL---SECCQ-----EVVD-----52
DB 30 VRDIERLISRNVPRLRRIGDAIQNMCMETNVSIRMYRQCKSESSDFVDEMLEHHENFIGS 89

QY 53 --TYGSSILSILIEVSPDLVCS 73
DB 90 SKSFASLLPLSVTFNTDMMACT 112

RESULT 9
US-11-194-246-316
; Sequence 316, Application US/11194246
; Publication No. US20050272089A1
; GENERAL INFORMATION:
; APPLICANT: Mott, John
; APPLICANT: Irepod, Catherine
; APPLICANT: Arvidson, Staffan
; TITLE OF INVENTION: CRITICAL GENES AND POLYPEPTIDES OF HAEMOPHILUS INFLUENZAE AND ME
; FILE REFERENCE: 00592.US1 (W&R 268.05920101)
; CURRENT APPLICATION NUMBER: US/11/194,246
; CURRENT FILING DATE: 2005-08-01
; PRIOR APPLICATION NUMBER: US/10/274,586
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US 60/345,438
; PRIOR FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 621
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 316
; LENGTH: 292
; TYPE: PRT
; ORGANISM: HAEMOPHILUS INFLUENZAE
US-11-194-246-316

Query Match          14.8%; Score 61; DB 7; Length 292;
Best Local Similarity 29.0%; Pred. No. 9;
Matches 20; Conservative 9; Mismatches 20; Indels 20; Gaps 3;

QY 12 VKEVTKL-----IDNNKT-----EKEILDADFCKMCKSLPKSLSECCQEVV-----51
DB 43 IASVTKLMTANVFLNNKPNCRIAITKEDTDRIKGTGTLKPKNIPISCNELLKAMLVHS 102

QY 52 DTYGSSILS 60
DB 103 DNYAAHALS 111

RESULT 10
US-11-124-368A-276
; Sequence 276, Application US/11124368A
; Publication No. US20050287559A1
; GENERAL INFORMATION:
; APPLICANT: Michele Cargill
; APPLICANT: James J. Devlin
```

```
; APPLICANT: May Luke
; TITLE OF INVENTION: Genetic Polymorphisms Associated with
; TITLE OF INVENTION: Vascular Diseases, Methods of Detection and Uses Thereof
; FILE REFERENCE: CL001524
; CURRENT APPLICATION NUMBER: US/11/124,368A
; CURRENT FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: US 60/568,845
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: US 60/625,936
; PRIOR FILING DATE: 2004-11-09
; NUMBER OF SEQ ID NOS: 21112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 276
; LENGTH: 2036
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-124-368A-276

Query Match      14.6%; Score 60; DB 7; Length 2036;
Best Local Similarity 25.3%; Pred. No. 1.2e+02;
Matches 20; Conservative 16; Mismatches 25; Indels 18; Gaps 3;

QY 17 KLIDNNKTEKILDAFDKMC-S-KLPKSLSEE-----CQEVVDYTGSSILSI 61
Db 281 KLDSAPATEAREPEWKEVCTIELRNGASQRPFPPLCNVDPDLITILHGISETYD---VSP 337

QY 62 LLEEVSPELVCSMLHLCSG 80
Db 338 LLHYMLPHLVVSIHHVTG 356

RESULT 11
US-11-124-368A-280
; Sequence 280, Application US/11124368A
; Publication No. US20050287559A1
; GENERAL INFORMATION:
; APPLICANT: Michele Cargill
; APPLICANT: James J. Devlin
; TITLE OF INVENTION: Genetic Polymorphisms Associated with
; TITLE OF INVENTION: Vascular Diseases, Methods of Detection and Uses Thereof
; FILE REFERENCE: CL001524
; CURRENT APPLICATION NUMBER: US/11/124,368A
; CURRENT FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: US 60/568,845
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: US 60/625,936
; PRIOR FILING DATE: 2004-11-09
; NUMBER OF SEQ ID NOS: 21112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 280
; LENGTH: 2036
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-124-368A-280

Query Match      14.6%; Score 60; DB 7; Length 2036;
Best Local Similarity 25.3%; Pred. No. 1.2e+02;
Matches 20; Conservative 16; Mismatches 25; Indels 18; Gaps 3;

QY 17 KLIDNNKTEKILDAFDKMC-S-KLPKSLSEE-----CQEVVDYTGSSILSI 61
Db 281 KLDSAPATEAREPEWKEVCTIELRNGASQRPFPPLCNVDPDLITILHGISETYD---VSP 337

QY 62 LLEEVSPELVCSMLHLCSG 80
Db 338 LLHYMLPHLVVSIHHVTG 356

RESULT 12
US-11-124-368A-281
; Sequence 281, Application US/11124368A
; Publication No. US20050287559A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Michele Cargill
; APPLICANT: James J. Devlin
; APPLICANT: May Luke
; TITLE OF INVENTION: Genetic Polymorphisms Associated with
; TITLE OF INVENTION: Vascular Diseases, Methods of Detection and Uses Thereof
; FILE REFERENCE: CL001524
; CURRENT APPLICATION NUMBER: US/11/124,368A
; CURRENT FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: US 60/568,845
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: US 60/625,936
; PRIOR FILING DATE: 2004-11-09
; NUMBER OF SEQ ID NOS: 21112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 281
; LENGTH: 2036
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-124-368A-281

Query Match      14.6%; Score 60; DB 7; Length 2036;
Best Local Similarity 25.3%; Pred. No. 1.2e+02;
Matches 20; Conservative 16; Mismatches 25; Indels 18; Gaps 3;

QY 17 KLIDNNKTEKILDAFDKMC-S-KLPKSLSEE-----CQEVVDYTGSSILSI 61
Db 281 KLDSAPATEAREPEWKEVCTIELRNGASQRPFPPLCNVDPDLITILHGISETYD---VSP 337

QY 62 LLEEVSPELVCSMLHLCSG 80
Db 338 LLHYMLPHLVVSIHHVTG 356

RESULT 13
US-10-821-234-916
; Sequence 916, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt SEQ_genes Version 1.0
; SEQ ID NO 916
; LENGTH: 3002
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-916

Query Match      14.4%; Score 59.5; DB 6; Length 3002;
Best Local Similarity 27.8%; Pred. No. 2.2e+02;
Matches 25; Conservative 8; Mismatches 30; Indels 27; Gaps 5;

QY 8 CBFL-----VKEVTKLIDNNKTEKEI-LDAFDKMC-S-KLPKSLSEEQOE- 49
Db 2627 CQFLCVNTIGGTCPCPFQHTTSCIDNNNECTSDINLCGSKGICQNTFGSFTCECQRG 2686

QY 50 -VVDYTGSSILSILLEEVSPELVCSMLHLC 78
Db 2687 FSLDQTGSS-----CEDVDE---CEGNHRC 2708

RESULT 14
US-09-940-308-3
; Sequence 3, Application US/09940308
```

```
; Publication No. US20040092437A1
; GENERAL INFORMATION:
; APPLICANT: Murgita, Robert A.
; TITLE OF INVENTION: Recombinant Human Alpha-Fetoprotein as
; TITLE OF INVENTION: an Immunosuppressive Agent
; FILE REFERENCE: 06727/005003
; CURRENT APPLICATION NUMBER: US/09/940,308
; CURRENT FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: US 09/186,723
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: US 08/377,309
; PRIOR FILING DATE: 1995-01-24
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 197
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-940-308-3
```

```
Query Match 14.3%; Score 59; DB 5; Length 197;
Best Local Similarity 35.1%; Pred.No. 9.3;
Matches 20; Conservative 10; Mismatches 21; Indels 6; Gaps 3;

Qy 7 VCEFLVKEVTKLIDNNKT--EKEILDADFDMC--SKLPKLSLSEC--QEVVDYTGSS 57
Db 36 VQEATYKEVSKWKVDALTATEKPTGDSGSGCLENQLPAFLLELCHEKEILEKYGHS 92
```

```
RESULT 15
US-09-940-308-6
; Sequence 6, Application US/09940308
; Publication No. US20040092437A1
; GENERAL INFORMATION:
; APPLICANT: Murgita, Robert A.
; TITLE OF INVENTION: Recombinant Human Alpha-Fetoprotein as
; TITLE OF INVENTION: an Immunosuppressive Agent
; FILE REFERENCE: 06727/005003
; CURRENT APPLICATION NUMBER: US/09/940,308
; CURRENT FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: US 09/186,723
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: US 08/377,309
; PRIOR FILING DATE: 1995-01-24
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 389
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-940-308-6
```

```
Query Match 14.3%; Score 59; DB 5; Length 389;
Best Local Similarity 35.1%; Pred.No. 21;
Matches 20; Conservative 10; Mismatches 21; Indels 6; Gaps 3;

Qy 7 VCEFLVKEVTKLIDNNKT--EKEILDADFDMC--SKLPKLSLSEC--QEVVDYTGSS 57
Db 36 VQEATYKEVSKWKVDALTATEKPTGDSGSGCLENQLPAFLLELCHEKEILEKYGHS 92
```

Search completed: January 13, 2006, 16:39:05
Job time : 1.5894 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 13, 2006, 16:26:00 ; Search time 8.34437 Seconds
(without alignments)
792.637 Million cell updates/sec

Title: US-10-801-517-2

Perfect score: 412

Sequence: 1 SDVYCEVCEPLVKEVTKLID.....ILLEEVSPENLVCMLHLCSG 80

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5 COMB.pap:*
2: /cgn2_6/ptodata/1/iaa/6 COMB.pap:*
3: /cgn2_6/ptodata/1/iaa/H COMB.pap:*
4: /cgn2_6/ptodata/1/iaa/PCRUS COMB.pap:*
5: /cgn2_6/ptodata/1/iaa/RE COMB.pap:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	412	100.0	80	1	US-08-100-247-3
2	412	100.0	80	1	US-08-483-146A-3
3	412	100.0	80	1	US-08-232-513A-4
4	412	100.0	80	1	US-08-484-594A-3
5	412	100.0	80	2	US-08-076-258A-3
6	412	100.0	80	2	US-08-756-031-3
7	412	100.0	80	2	US-08-928-074-24
8	412	100.0	523	1	US-08-100-247-2
9	412	100.0	523	1	US-08-483-146A-2
10	412	100.0	523	1	US-08-232-513A-3
11	412	100.0	523	1	US-08-484-594A-2
12	412	100.0	523	2	US-09-076-258A-2
13	412	100.0	523	2	US-08-756-031-2
14	412	100.0	524	2	US-09-352-548-1
15	412	100.0	524	2	US-09-949-016-6272
16	412	100.0	524	2	US-08-928-074-23
17	412	100.0	535	2	US-09-949-016-8603
18	211	51.2	40	2	US-09-780-438C-1
19	201	48.8	38	2	US-09-780-438C-2
20	111	26.9	22	1	US-08-100-247-1
21	111	26.9	22	1	US-08-483-146A-1
22	111	26.9	22	1	US-08-232-513A-1
23	111	26.9	22	1	US-08-484-594A-1
24	111	26.9	22	2	US-09-231-159-1
25	111	26.9	22	2	US-08-611-307-1
26	111	26.9	22	2	US-09-148-030-1
27	111	26.9	22	2	US-09-076-258A-1

28	111	26.9	22	2	US-08-756-031-1	Sequence 1, Appli
29	111	26.9	22	2	US-08-928-074-1	Sequence 1, Appli
30	106	25.7	22	2	US-09-231-159-8	Sequence 8, Appli
31	106	25.7	22	2	US-08-611-307-8	Sequence 8, Appli
32	106	25.7	22	2	US-08-928-074-8	Sequence 8, Appli
33	101	24.5	38	2	US-09-780-438C-3	Sequence 3, Appli
34	101	24.5	38	2	US-09-780-438C-5	Sequence 5, Appli
35	101	24.5	38	2	US-09-780-438C-6	Sequence 6, Appli
36	101	24.5	39	2	US-09-780-438C-4	Sequence 4, Appli
37	96	23.3	22	1	US-08-483-146A-9	Sequence 9, Appli
38	96	23.3	22	1	US-08-232-513A-18	Sequence 18, Appli
39	96	23.3	22	1	US-08-484-594A-9	Sequence 9, Appli
40	96	23.3	22	2	US-09-231-159-7	Sequence 7, Appli
41	96	23.3	22	2	US-08-611-307-7	Sequence 7, Appli
42	96	23.3	22	2	US-09-076-258A-9	Sequence 9, Appli
43	96	23.3	22	2	US-08-928-074-7	Sequence 7, Appli
44	96	23.3	514	2	US-10-339-351-2	Sequence 2, Appli
45	92	22.3	79	2	US-08-596-684F-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-08-100-247-3
; Sequence 3, Application US/08100247
; Patent No. 5571787
; GENERAL INFORMATION:
; APPLICANT: O'BRIEN, JOHN S.
; APPLICANT: KISHIMOTO, YASUO
; TITLE OF INVENTION: PROSAPOSIN AS A NEUTROTROPIC FACTOR
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: KNOBBE, MARTENS, OLSON AND BEAR
; STREET: 620 NEWPORT CENTER DRIVE SIXTEENTH FLOOR
; CITY: NEWPORT BEACH
; STATE: CA
; COUNTRY: USA
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/100,247
; FILING DATE: 19930730
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Israelaen, Ned A.
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: OBRIEN.002A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-235-8550
; TELEFAX: 619-235-0176
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 80 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; IMMEDIATE SOURCE:
; CLONE: SAPOSIN C
; US-08-100-247-3

Query Match 100.0%; Score 412; DB 1; Length 80;
Best Local Similarity 100.0%; Pred. No. 6.9e-42;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 SDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDKMCCKLPKSLSECEQVVDVTYSSILS 60
Db 1 SDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDKMCCKLPKSLSECEQVVDVTYSSILS 60
QY 61 ILLEEVSPELVCSMLHLCSG 80
Db 61 ILLEEVSPELVCSMLHLCSG 80

RESULT 2
US-08-483-146A-3
; Sequence 3, Application US/08483146A
; Patent No. 5696080
; GENERAL INFORMATION:
; APPLICANT: O'Brien, John S.
; APPLICANT: Kishimoto, Yasuo
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS
; TITLE OF INVENTION: COMPRISING PROSAPOSIN AND NEUROTROPHIC PEPTIDES DERIVED
; TITLE OF INVENTION: THEREFROM
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson and Bear
; STREET: 620 Newport Center Blvd. 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,146A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Israelsen, Ned A
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: MYELOS.002DV1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-235-8550
; TELEFAX: 619-235-0176
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 80 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-08-483-146A-3

Query Match 100.0%; Score 412; DB 1; Length 80;
Best Local Similarity 100.0%; Pred. No. 6.9e-42;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDKMCCKLPKSLSECEQVVDVTYSSILS 60
Db 1 SDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDKMCCKLPKSLSECEQVVDVTYSSILS 60
QY 61 ILLEEVSPELVCSMLHLCSG 80
Db 61 ILLEEVSPELVCSMLHLCSG 80

RESULT 3
US-08-232-513A-4
; Sequence 4, Application US/08232513A
```

```
; Patent No. 5700909
; GENERAL INFORMATION:
; APPLICANT: O'Brien, John S.
; TITLE OF INVENTION: Prosaposin and Cytokine-Derived Peptides
; TITLE OF INVENTION: as Therapeutic Agents
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,513A
; FILING DATE: 21-APR-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/100,247
; FILING DATE: 30-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UD 1643
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 80 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..80
; OTHER INFORMATION: /label= Saposin_C
; US-08-232-513A-4

Query Match 100.0%; Score 412; DB 1; Length 80;
Best Local Similarity 100.0%; Pred. No. 6.9e-42;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDKMCCKLPKSLSECEQVVDVTYSSILS 60
Db 1 SDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDKMCCKLPKSLSECEQVVDVTYSSILS 60
QY 61 ILLEEVSPELVCSMLHLCSG 80
Db 61 ILLEEVSPELVCSMLHLCSG 80

RESULT 4
US-08-484-594A-3
; Sequence 3, Application US/08484594A
; Patent No. 5714459
; GENERAL INFORMATION:
; APPLICANT: O'Brien, John S.
; APPLICANT: Kishimoto, Yasuo
; TITLE OF INVENTION: USE OF PROSAPOSIN AND NEUROTROPHIC PEPTIDES
; TITLE OF INVENTION: DERIVED THEREFROM
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson and Bear
; STREET: 620 Newport Center Drive, Sixteenth Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
```

```

; FILING DATE: 28-OCT-97
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/483,146
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: 08/100,247
; FILING DATE: 30-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Israelsen, Ned A
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: MYELOS.2DV1C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-235-8550
; TELEFAX: 619-235-0176
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 80 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-09-076-258A-3
;
; Query Match 100.0%; Score 412; DB 2; Length 80;
; Best Local Similarity 100.0%; Pred. No. 6.9e-42;
; Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 1 SDVCEVCFVLKVEVTKLIDNNKTEKILDAPDKMCKLPKSLSEECQEVVDYTGSSILS 60
; DB 1 SDVCEVCFVLKVEVTKLIDNNKTEKILDAPDKMCKLPKSLSEECQEVVDYTGSSILS 60
;
; QY 61 ILLEEVSPELVCMLHLCSG 80
; DB 61 ILLEEVSPELVCMLHLCSG 80
;
; RESULT 6
; US-08-756-031-3
; Sequence 3, Application US/08756031
; Patent No. 6590074
; GENERAL INFORMATION:
; APPLICANT: O'BRIEN, JOHN S.
; APPLICANT: KISHIMOTO, YASUO
; TITLE OF INVENTION: PROSAPOSIN AS A NEUTROTROPHIC FACTOR
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESS: KNOBBE, MARTENS, OLSON AND BEAR
; STREET: 620 NEWPORT CENTER DRIVE SIXTEENTH FLOOR
; CITY: NEWPORT BEACH
; STATE: CA
; COUNTRY: USA
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/756,031
; FILING DATE: 26-NOV-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/100,247
; FILING DATE: 30-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Israelsen, Ned A.
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: OBRIEN.002A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-235-8550
; TELEFAX: 619-235-0176
; INFORMATION FOR SEQ ID NO: 3:

```

QY	1	SDVYCEVCEFLVKEVT	KLIDNNKTEKILDAFDMKCSKLPKSLSEECQEVVDVTYGS	ILS	60
QY	1	SDVYCEVCEFLVKEVT	KLIDNNKTEKILDAFDMKCSKLPKSLSEECQEVVDVTYGS	ILS	60
Db	1	SDVYCEVCEFLVKEVT	KLIDNNKTEKILDAFDMKCSKLPKSLSEECQEVVDVTYGS	ILS	60
QY	61	ILLEVSPELVCSMLHLC	SG	80	
Db	61	ILLEVSPELVCSMLHLC	SG	80	
<p>RESULT 8</p> <p>US-08-100-247-2</p> <p>Query Match 100.0%; Score 412; DB 2; Length 80;</p> <p>Best Local Similarity 100.0%; Pred. No. 6.9e-42;</p> <p>Mismatches 0; Conservative 0; Indels 0; Gaps 0;</p> <p>GENERAL INFORMATION:</p> <p>APPLICANT: O'BRIEN, JOHN S.</p> <p>APPLICANT: KISHIMOTO, YASUO</p> <p>TITLE OF INVENTION: PROSAPOSIN AS A NEUROTROPIC FACTOR</p> <p>NUMBER OF SEQUENCES: 5</p> <p>CORRESPONDENCE ADDRESS:</p> <p>ADDRESSEE: KNOBBE, MARTENS, OLSON AND BEAR</p> <p>STREET: 620 NEWPORT CENTER DRIVE</p> <p>CITY: NEWPORT BEACH</p> <p>STATE: CA</p> <p>COUNTRY: USA</p> <p>ZIP: 92660</p> <p>COMPUTER READABLE FORM:</p> <p>MEDIUM TYPE: Floppy disk</p> <p>COMPUTER: IBM PC compatible</p> <p>OPERATING SYSTEM: PC-DOS/MS-DOS</p> <p>SOFTWARE: Patent In Release #1.0, Version #1.25</p> <p>CURRENT APPLICATION DATA:</p> <p>APPLICATION NUMBER: US/08/100,247</p> <p>FILING DATE: 19930730</p> <p>CLASSIFICATION: 514</p> <p>ATTORNEY/AGENT INFORMATION:</p> <p>NAME: Israel, Ned A.</p> <p>REGISTRATION NUMBER: 29,655</p> <p>REFERENCE/DOCKET NUMBER: O'BRIEN.002A</p> <p>TELECOMMUNICATION INFORMATION:</p> <p>TELEPHONE: 619-235-8550</p> <p>TELEFAX: 619-235-0176</p> <p>INFORMATION FOR SEQ ID NO: 2:</p> <p>SEQUENCE CHARACTERISTICS:</p> <p>LENGTH: 523 amino acids</p> <p>TYPE: amino acid</p> <p>STRANDEDNESS: single</p> <p>TOPOLOGY: linear</p> <p>MOLECULE TYPE: peptide</p> <p>HYPOTHEICAL: NO</p> <p>ANTI-SENSE: NO</p> <p>FRAGMENT TYPE: N-terminal</p> <p>IMMEDIATE SOURCE:</p> <p>CLONE: PROSAPOSIN</p> <p>US-08-100-247-2</p>					
QY	1	SDVYCEVCEFLVKEVT <th>KLIDNNKTEKILDAFDMKCSKLPKSLSEECQEVVDVTYGS</th> <th>ILS</th> <th>60</th>	KLIDNNKTEKILDAFDMKCSKLPKSLSEECQEVVDVTYGS	ILS	60
Db	310	SDVYCEVCEFLVKEVT <th>KLIDNNKTEKILDAFDMKCSKLPKSLSEECQEVVDVTYGS</th> <th>ILS</th> <th>366</th>	KLIDNNKTEKILDAFDMKCSKLPKSLSEECQEVVDVTYGS	ILS	366
QY	61	ILLEVSPELVCSMLHLC	SG	80	
Db	370	ILLEVSPELVCSMLHLC	SG	389	
<p>RESULT 9</p> <p>US-08-483-146A-2</p> <p>Query Match 100.0%; Score 412; DB 1; Length 523;</p> <p>Best Local Similarity 100.0%; Pred. No. 8e-41;</p> <p>Mismatches 0; Conservative 0; Indels 0; Gaps 0;</p> <p>GENERAL INFORMATION:</p> <p>APPLICANT: O'BRIEN, JOHN S.</p> <p>APPLICANT: KISHIMOTO, YASUO</p> <p>TITLE OF INVENTION: PROSAPOSIN AS A NEUROTROPIC FACTOR</p> <p>NUMBER OF SEQUENCES: 5</p> <p>CORRESPONDENCE ADDRESS:</p> <p>ADDRESSEE: KNOBBE, MARTENS, OLSON AND BEAR</p> <p>STREET: 620 NEWPORT CENTER DRIVE</p> <p>CITY: NEWPORT BEACH</p> <p>STATE: CA</p> <p>COUNTRY: USA</p> <p>ZIP: 92660</p> <p>COMPUTER READABLE FORM:</p> <p>MEDIUM TYPE: Floppy disk</p> <p>COMPUTER: IBM PC compatible</p> <p>OPERATING SYSTEM: PC-DOS/MS-DOS</p> <p>SOFTWARE: Patent In Release #1.0, Version #1.25</p> <p>CURRENT APPLICATION DATA:</p> <p>APPLICATION NUMBER: US/08/100,247</p> <p>FILING DATE: 19930730</p> <p>CLASSIFICATION: 514</p> <p>ATTORNEY/AGENT INFORMATION:</p> <p>NAME: Israel, Ned A.</p> <p>REGISTRATION NUMBER: 29,655</p> <p>REFERENCE/DOCKET NUMBER: O'BRIEN.002A</p> <p>TELECOMMUNICATION INFORMATION:</p> <p>TELEPHONE: 619-235-8550</p> <p>TELEFAX: 619-235-0176</p> <p>INFORMATION FOR SEQ ID NO: 2:</p> <p>SEQUENCE CHARACTERISTICS:</p> <p>LENGTH: 523 amino acids</p> <p>TYPE: amino acid</p> <p>STRANDEDNESS: single</p> <p>TOPOLOGY: linear</p> <p>MOLECULE TYPE: peptide</p> <p>HYPOTHEICAL: NO</p> <p>ANTI-SENSE: NO</p> <p>FRAGMENT TYPE: N-terminal</p> <p>IMMEDIATE SOURCE:</p> <p>CLONE: PROSAPOSIN</p> <p>US-08-100-247-2</p>					
QY	1	SDVYCEVCEFLVKEVT <th>KLIDNNKTEKILDAFDMKCSKLPKSLSEECQEVVDVTYGS</th> <th>ILS</th> <th>60</th>	KLIDNNKTEKILDAFDMKCSKLPKSLSEECQEVVDVTYGS	ILS	60
Db	310	SDVYCEVCEFLVKEVT <th>KLIDNNKTEKILDAFDMKCSKLPKSLSEECQEVVDVTYGS</th> <th>ILS</th> <th>366</th>	KLIDNNKTEKILDAFDMKCSKLPKSLSEECQEVVDVTYGS	ILS	366
QY	61	ILLEVSPELVCSMLHLC	SG	80	
Db	370	ILLEVSPELVCSMLHLC	SG	389	
<p>RESULT 9</p> <p>US-08-483-146A-2</p> <p>Query Match 100.0%; Score 412; DB 2; Length 80;</p> <p>Best Local Similarity 100.0%; Pred. No. 6.9e-42;</p> <p>Mismatches 0; Conservative 0; Indels 0; Gaps 0;</p> <p>GENERAL INFORMATION:</p> <p>APPLICANT: O'BRIEN, JOHN S.</p> <p>APPLICANT: KISHIMOTO, YASUO</p> <p>TITLE OF INVENTION: PROSAPOSIN AS A NEUROTROPIC FACTOR</p> <p>NUMBER OF SEQUENCES: 5</p> <p>CORRESPONDENCE ADDRESS:</p> <p>ADDRESSEE: KNOBBE, MARTENS, OLSON AND BEAR</p> <p>STREET: 620 NEWPORT CENTER DRIVE</p> <p>CITY: NEWPORT BEACH</p> <p>STATE: CA</p> <p>COUNTRY: USA</p> <p>ZIP: 92660</p> <p>COMPUTER READABLE FORM:</p> <p>MEDIUM TYPE: Floppy disk</p> <p>COMPUTER: IBM PC compatible</p> <p>OPERATING SYSTEM: PC-DOS/MS-DOS</p> <p>SOFTWARE: Patent In Release #1.0, Version #1.25</p> <p>CURRENT APPLICATION DATA:</p> <p>APPLICATION NUMBER: US/08/100,247</p> <p>FILING DATE: 19930730</p> <p>CLASSIFICATION: 514</p> <p>ATTORNEY/AGENT INFORMATION:</p> <p>NAME: Israel, Ned A.</p> <p>REGISTRATION NUMBER: 29,655</p> <p>REFERENCE/DOCKET NUMBER: O'BRIEN.002A</p> <p>TELECOMMUNICATION INFORMATION:</p> <p>TELEPHONE: 619-235-8550</p> <p>TELEFAX: 619-235-0176</p> <p>INFORMATION FOR SEQ ID NO: 2:</p> <p>SEQUENCE CHARACTERISTICS:</p> <p>LENGTH: 523 amino acids</p> <p>TYPE: amino acid</p> <p>STRANDEDNESS: single</p> <p>TOPOLOGY: linear</p> <p>MOLECULE TYPE: peptide</p> <p>HYPOTHEICAL: NO</p> <p>ANTI-SENSE: NO</p> <p>FRAGMENT TYPE: N-terminal</p> <p>IMMEDIATE SOURCE:</p> <p>CLONE: PROSAPOSIN</p> <p>US-08-100-247-2</p>					
QY	1	SDVYCEVCEFLVKEVT <th>KLIDNNKTEKILDAFDMKCSKLPKSLSEECQEVVDVTYGS</th> <th>ILS</th> <th>60</th>	KLIDNNKTEKILDAFDMKCSKLPKSLSEECQEVVDVTYGS	ILS	60
Db	310	SDVYCEVCEFLVKEVT <th>KLIDNNKTEKILDAFDMKCSKLPKSLSEECQEVVDVTYGS</th> <th>ILS</th> <th>366</th>	KLIDNNKTEKILDAFDMKCSKLPKSLSEECQEVVDVTYGS	ILS	366
QY	61	ILLEVSPELVCSMLHLC	SG	80	
Db	370	ILLEVSPELVCSMLHLC	SG	389	
<p>RESULT 9</p> <p>US-08-483-146A-2</p> <p>Query Match 100.0%; Score 412; DB 2; Length 80;</p> <p>Best Local Similarity 100.0%; Pred. No. 6.9e-42;</p> <p>Mismatches 0; Conservative 0; Indels 0; Gaps 0;</p> <p>GENERAL INFORMATION:</p> <p>APPLICANT: O'BRIEN, JOHN S.</p> <p>APPLICANT: KISHIMOTO, YASUO</p> <p>TITLE OF INVENTION: PROSAPOSIN AS A NEUROTROPIC FACTOR</p> <p>NUMBER OF SEQUENCES: 5</p> <p>CORRESPONDENCE ADDRESS:</p> <p>ADDRESSEE: KNOBBE, MARTENS, OLSON AND BEAR</p> <p>STREET: 620 NEWPORT CENTER DRIVE</p> <p>CITY: NEWPORT BEACH</p> <p>STATE: CA</p> <p>COUNTRY: USA</p> <p>ZIP: 92660</p> <p>COMPUTER READABLE FORM:</p> <p>MEDIUM TYPE: Floppy disk</p> <p>COMPUTER: IBM PC compatible</p> <p>OPERATING SYSTEM: PC-DOS/MS-DOS</p> <p>SOFTWARE: Patent In Release #1.0, Version #1.25</p> <p>CURRENT APPLICATION DATA:</p> <p>APPLICATION NUMBER: US/08/100,247</p> <p>FILING DATE: 19930730</p> <p>CLASSIFICATION: 514</p> <p>ATTORNEY/AGENT INFORMATION:</p> <p>NAME: Israel, Ned A.</p> <p>REGISTRATION NUMBER: 29,655</p> <p>REFERENCE/DOCKET NUMBER: O'BRIEN.002A</p> <p>TELECOMMUNICATION INFORMATION:</p> <p>TELEPHONE: 619-235-8550</p> <p>TELEFAX: 619-235-0176</p> <p>INFORMATION FOR SEQ ID NO: 2:</p> <p>SEQUENCE CHARACTERISTICS:</p> <p>LENGTH: 523 amino acids</p> <p>TYPE: amino acid</p> <p>STRANDEDNESS: single</p> <p>TOPOLOGY: linear</p> <p>MOLECULE TYPE: peptide</p> <p>HYPOTHEICAL: NO</p> <p>ANTI-SENSE: NO</p> <p>FRAGMENT TYPE: N-terminal</p> <p>IMMEDIATE SOURCE:</p> <p>CLONE: PROSAPOSIN</p> <p>US-08-100-247-2</p>					
QY	1	SDVYCEVCEFLVKEVT <th>KLIDNNKTEKILDAFDMKCSKLPKSLSEECQEVVDVTYGS</th> <th>ILS</th> <th>60</th> </	KLIDNNKTEKILDAFDMKCSKLPKSLSEECQEVVDVTYGS	ILS	60

```

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,513A
FILING DATE: 21-APR-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/100,247
FILING DATE: 30-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UD 1643
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 523 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..523
OTHER INFORMATION: /label= Hum_prosaposin
US-08-232-513A-3

Query Match 100.0%; Score 412; DB 1; Length 523;
Best Local Similarity 100.0%; Pred. No. 8e-41;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Qy 1 SDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDKWC SKLPKSLSECEVVDVTYGSSTLS 60
Db 310 SDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDKWC SKLPKSLSECEVVDVTYGSSTLS 369

Qy 61 ILLEEVSPELVCSMLHLCSG 80
Db 370 ILLEEVSPELVCSMLHLCSG 389

RESULT 11
US-08-484-594A-2
Sequence 2, Application US/08484594A
Patent No. 5714459
GENERAL INFORMATION:
APPLICANT: O'Brien, John S.
APPLICANT: Kishimoto, Yasuo
TITLE OF INVENTION: USE OF PROSAPOSIN AND NEUROTROPHIC PEPTIDES
TITLE OF INVENTION: DERIVED THEREFROM
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson and Bear
STREET: 620 Newport Center Drive, Sixteenth Floor
CITY: Newport Beach
STATE: CA
COUNTRY: USA
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,594A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/100,247
FILING DATE: 30-JUL-1993

```

Wed Jan 18 11:58:42 2006

```

;
; ATTORNEY/AGENT INFORMATION:
; NAME: Israelsen, Ned A
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: MYELOS.002DV2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-235-8550
; TELEFAX: 619-235-0176
;
; TELEX:
;
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 523 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: N-terminal
;
US-08-484-594A-2
;
Query Match 100.0%; Score 412; DB 1; Length 523;
Best Local Similarity 100.0%; Pred. No. 8e-41;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDKMCCKLPKSLSECEQVVDVYGGSSILS 60
Db 310 SDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDKMCCKLPKSLSECEQVVDVYGGSSILS 369

QY 61 ILLEEVSPELVCSMLHLCSG 80
Db 370 ILLEEVSPELVCSMLHLCSG 389

RESULT 12
US-09-076-258A-2
; Sequence 2, Application US/09076258A
; Patent No. 6559124
;
; GENERAL INFORMATION:
; APPLICANT: O'Brien, John S.
; APPLICANT: Kishimoto, Yasuo
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS
; TITLE OF INVENTION: COMPRISING PROSAPOSIN AND NEUROTROPHIC PEPTIDES DERIVED
; TITLE OF INVENTION: THEREFROM
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson and Bear
; STREET: 620 Newport Center Blvd. 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/076,258A
; FILING DATE:
; CLASSIFICATION:
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/956,970
; FILING DATE: 28-OCT-97
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/483,146
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: 08/100,247
; FILING DATE: 30-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Israelsen, Ned A
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: MYELOS.2DVLC2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-235-8550
; TELEFAX: 619-235-0176
;

```

```

;
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 523 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: N-terminal
;
US-09-076-258A-2
;
Query Match 100.0%; Score 412; DB 2; Length 523;
Best Local Similarity 100.0%; Pred. No. 8e-41;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDKMCCKLPKSLSECEQVVDVYGGSSILS 60
Db 310 SDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDKMCCKLPKSLSECEQVVDVYGGSSILS 369

QY 61 ILLEEVSPELVCSMLHLCSG 80
Db 370 ILLEEVSPELVCSMLHLCSG 389

RESULT 13
US-08-756-031-2
; Sequence 2, Application US/08756031
; Patent No. 6590074
;
; GENERAL INFORMATION:
; APPLICANT: O'Brien, John S.
; APPLICANT: Kishimoto, Yasuo
; TITLE OF INVENTION: PROSAPOSIN AS A NEUROTROPHIC FACTOR
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson and Bear
; STREET: 620 Newport Center Drive Sixteenth Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/756,031
; FILING DATE: 26-NOV-1996
; CLASSIFICATION: 514
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/100,247
; FILING DATE: 30-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Israelsen, Ned A.
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: O'BRIEN.002A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-235-8550
; TELEFAX: 619-235-0176
;
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 523 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; IMMEDIATE SOURCE:
; CLONE: PROSAPOSIN
;
US-08-756-031-2
;

```

```
Query Match      100.0%; Score 412; DB 2; Length 523;
Best Local Similarity 100.0%; Pred. No. 8e-41;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SDVYCEVCEFLVKEVTGLIDNNKTEKILDAFDKMCCKLPKSLSEECQEVVDYTGSSILS 60
    |||||
Db 310 SDVYCEVCEFLVKEVTGLIDNNKTEKILDAFDKMCCKLPKSLSEECQEVVDYTGSSILS 369
    |||||

Qy 61 ILLEVSPELVCSMLHLCSG 80
    |||||
Db 370 ILLEVSPELVCSMLHLCSG 389
    |||||

RESULT 14
US-09-352-548-1
; Sequence 1, Application US/09352548
; Patent No. 6500431
; GENERAL INFORMATION:
; APPLICANT: Parkash S. Gill, M.D., Inc.
; TITLE OF INVENTION: No. 6500431el Inhibitors of Angiogenesis and Tumor Growth
; FILE REFERENCE: 017986-000410US
; CURRENT APPLICATION NUMBER: US/09/352,548
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: US 60/092,647
; EARLIER FILING DATE: 1998-07-13
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 524
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: prosaposin
; NAME/KEY: PEPTIDE
; LOCATION: (195)..(275)
; OTHER INFORMATION: Saposin B
US-09-352-548-1

Query Match      100.0%; Score 412; DB 2; Length 524;
Best Local Similarity 100.0%; Pred. No. 8e-41;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SDVYCEVCEFLVKEVTGLIDNNKTEKILDAFDKMCCKLPKSLSEECQEVVDYTGSSILS 60
    |||||
Db 311 SDVYCEVCEFLVKEVTGLIDNNKTEKILDAFDKMCCKLPKSLSEECQEVVDYTGSSILS 370
    |||||

Qy 61 ILLEVSPELVCSMLHLCSG 80
    |||||
Db 371 ILLEVSPELVCSMLHLCSG 390
    |||||

RESULT 15
US-09-949-016-6272
; Sequence 6272, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6272
```

```
; LENGTH: 524
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6272

Query Match      100.0%; Score 412; DB 2; Length 524;
Best Local Similarity 100.0%; Pred. No. 8e-41;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SDVYCEVCEFLVKEVTGLIDNNKTEKILDAFDKMCCKLPKSLSEECQEVVDYTGSSILS 60
    |||||
Db 311 SDVYCEVCEFLVKEVTGLIDNNKTEKILDAFDKMCCKLPKSLSEECQEVVDYTGSSILS 370
    |||||

Qy 61 ILLEVSPELVCSMLHLCSG 80
    |||||
Db 371 ILLEVSPELVCSMLHLCSG 390
    |||||

Search completed: January 13, 2006, 16:36:34
Job time : 8.34437 secs
```

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 13, 2006, 16:23:49 ; Search time 6.35762 Seconds
(without alignments)
1210.728 Million cell updates/sec

Title: US-10-801-517-2

Perfect score: 412

Sequence: 1 SDVYCVCEFLVKEVTKLID.....ILLERVSPELVCSMLHLCSS 80

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 80.*

1: Pir1.*

2: Pir2.*

3: Pir3.*

4: Pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	412	100.0	527	1 SAHUP	saposin precursor
2	343	83.3	80	2 S21770	saposin-C - bovine
3	261	63.3	81	2 A32026	glucosylceramide b
4	193	46.8	554	1 A28716	saposin precursor
5	168	40.8	557	1 JH0604	saposin precursor
6	158	38.3	965	2 T00207	p109 protein - sil
7	106.5	25.8	217	2 T48201	hypothetical prote
8	106	25.7	213	2 T46069	hypothetical prote
9	106	25.7	428	2 S47096	cynarase (EC 3.4.2
10	106	25.7	474	2 T12049	cyprosin (EC 3.4.2
11	104	25.2	506	2 F86253	hypothetical prote
12	103	25.0	292	2 T14446	aspartic proteinas
13	103	25.0	322	2 S41400	aspartic proteinas
14	103	25.0	433	2 E96649	hypothetical prote
15	102.5	24.9	376	2 S02766	pulmonary surfacta
16	102	24.8	506	2 T07915	probable aspartic
17	102	24.8	509	2 JC7272	aspartic proteinas
18	100	24.3	513	2 T11686	aspartic proteinas
19	99.5	24.2	103	2 D89587	protein T08A9.8 [i
20	99.5	24.2	363	2 A29072	pulmonary surfacta
21	99	24.0	575	1 A40292	acyloxacyl hydrol
22	98	23.8	496	2 J50732	aspartic proteinas
23	97	23.5	508	2 S19697	aspartic proteinas
24	97	23.5	509	2 S66516	oryzaein (EC 3.4.2
25	97	23.5	513	2 T09739	aspartic endopepti
26	96.5	23.4	101	1 S49145	amoebapore C precu
27	95	23.1	79	1 LNP61	pulmonary surfacta
28	95	23.1	369	2 T46531	surfactant protein
29	92	22.3	509	2 S49349	cyprosin (EC 3.4.2

30	91	22.1	370	1 LNRBB	pulmonary surfacta
31	91	22.1	381	1 LNHUB	pulmonary surfacta
32	91	22.1	508	2 D85056	probable aspartic
33	90.5	22.0	96	1 S49144	amoebapore B precu
34	90.5	22.0	98	1 S25283	amoebapore A precu
35	89.5	21.7	205	2 B89567	protein T08A9.7 [i
36	89	21.6	314	2 T15674	hypothetical prote
37	87	21.1	195	2 T15676	hypothetical prote
38	84.5	20.5	129	2 S50444	NK-lysin protein -
39	82.5	20.0	280	2 PC4080	aspartic proteinas
40	81.5	19.8	223	2 B89567	protein T08A9.9 [i
41	79	19.2	650	2 T06617	endostyle-specific
42	78.5	19.1	74	2 C89567	protein T08A9.10 [
43	78	18.9	506	2 S71591	aspartic proteinas
44	77.5	18.8	572	2 T27869	sphingomyelin phos
45	76	18.4	306	2 T09915	hypothetical prote

ALIGNMENTS

RESULT 1

SAHUP

saposin precursor [validated] - human

N;Alternate names: cerebroside sulfate activator protein; co-beta-glucosidase; componen
ein (SAP); sphingolipid activator protein A2; sulfate activator protein
N;Contains: prosaposin; saposin A; saposin B; saposin C; saposin D
C;Species: Homo sapiens (man)

C;Date: 30-Jun-1992 #sequence_revision 17-Nov-1995 #text change 09-Jul-2004

C;Accession: JX0061; A57368; A42003; B42003; C42003; D42003; A30367; S34740; S36140; S3
0226; I37265; I37264

R;Nakano, T.; Sandhoff, K.; Stuempert, J.; Christomanou, H.; Suzuki, K.

J. Biochem. 105, 152-154, 1989

A;Title: Structure of full-length cDNA coding for sulfate activator, a Co-beta-glucos
A;Reference number: JX0061; MUID:89255151; PMID:2498298

A;Accession: JX0061

A;Molecule type: mRNA

A;Residues: 1-527 <NA>

A;Cross-references: UNIPROT:P07602; UNIPARC:UPI000002B33D; GB:D00422; NID:g220063; PIDN

A;Note: alternative splice form 1

A;Accession: A57368

A;Molecule type: mRNA

A;Residues: 1-259,263-527 <NA2>

A;Cross-references: UNIPARC:UPI0000000DBF; GB:J03015; GB:J03086; NID:g337755; PIDN:AAB5

A;Note: alternative splice form 2

R;Rorman, E.G.; Scheinker, V.; Grabowski, G.A.

Genomics 13, 312-318, 1992

A;Title: Structure and evolution of the human prosaposin chromosomal gene.

A;Reference number: A42003; MUID:92307663; PMID:1612590

A;Accession: A42003

A;Molecule type: DNA

A;Residues: 50-140 <ROR>

A;Cross-references: UNIPARC:UPI00001741AA; GB:M86181

A;Note: sequence extracted from NCBI backbone (NCBIN:107235, NCBIIP:107236)

A;Accession: B42003

A;Molecule type: DNA

A;Residues: 185-259,263-276 <RO2>

A;Cross-references: UNIPARC:UPI00001741AB; UNIPARC:UPI00001741AC

A;Note: sequence extracted from NCBI backbone (NCBIN:107235, NCBIIP:107237)

A;Accession: C42003

A;Molecule type: DNA

A;Residues: 305-393 <RO3>

A;Cross-references: UNIPARC:UPI00001741AD

A;Note: sequence extracted from NCBI backbone (NCBIN:107235, NCBIIP:107238); sequence in

A;Accession: D42003

A;Molecule type: DNA

A;Residues: 399-487 <RO4>

A;Cross-references: UNIPARC:UPI00001741AE

A;Note: sequence extracted from NCBI backbone (NCBIN:107235, NCBIIP:107239); sequence in

R;Rorman, E.G.; Grabowski, G.A.

Genomics 5, 486-492, 1989

A;Title: Molecular cloning of a human co-beta-glucosidase cDNA: evidence that four sphi

A;Reference number: A30367; MUID:90129043; PMID:2515150

A;Accession: A30367
A;Molecule type: mRNA
A;Residues: 1-259,263-527 <ROS>
A;Cross-references: UNIPARC:UPI00000000DBF; GB:J03077; NID:g183230; PIDN:AAA52560.1; PID:
A;Note: alternative splice form 2
R;Hiraiwa, M.; O'Brien, J.S.; Kishimoto, Y.; Galdzicka, M.; Fluharty, A.L.; Ginns, E.I.;
Arch. Biochem. Biophys. 304, 110-116, 1993
A;Title: Isolation, characterization, and proteolysis of human prosaposin, the precursor
A;Reference number: S34740; MUID:93311991; PMID:8323276
A;Accession: S34740
A;Molecule type: protein
A;Residues: 17-24;165-172;180-189;301-305 <HIR>
A;Cross-references: UNIPARC:UPI00001741AF; UNIPARC:UPI00001741B0; UNIPARC:UPI00001741B1;
R;Tyynelae, J.; Palmer, D.N.; Baumann, M.; Haltia, M.
FEBS Lett. 330, 8-12, 1993
A;Title: Storage of saposins A and D in infantile neuronal ceroid-lipofuscinosis.
A;Reference number: S36140; MUID:93380576; PMID:8370464
A;Accession: S36140
A;Molecule type: protein
A;Residues: 'XX',62,'X',64-65,'X',67-79,'X',81-84 <TY>
A;Cross-references: UNIPARC:UPI00001741B3
A;Note: saposin A
A;Accession: S36141
A;Molecule type: protein
A;Residues: 'XX',413-414,'X',416-428,'X',430-434 <TY2>
A;Cross-references: UNIPARC:UPI00001741B4
A;Note: saposin D
R;Holschmidt, H.; Sandhoff, K.; Kwon, H.Y.; Harzer, K.; Nakano, T.; Suzuki, K.
J. Biol. Chem. 266, 7556-7560, 1991
A;Title: Sulfatide activator protein. Alternative splicing that generates three mRNAs and
A;Reference number: S36988; MUID:91210267; PMID:2019586
A;Accession: S36988
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-240,'S',242-257 <HOL>
A;Cross-references: UNIPARC:UPI000016AFP6; EMBL:M60255; NID:g337759; PIDN:AAA36594.1; PI
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1991
A;Note: cerebroside sulfate activator protein mutant MU-9; corresponds to alternative sp
A;Accession: S36989
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-240,'S',242-259,263-527 <HO2>
A;Cross-references: UNIPARC:UPI000016AFP7; EMBL:M60257; NID:g337764; PIDN:AAA36595.1; PI
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1991
A;Note: cerebroside sulfate activator protein mutant MU-0; corresponds to alternative sp
A;Accession: S36990
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-240,'S',242-259,261-527 <HO3>
A;Cross-references: UNIPARC:UPI000016AFP8; EMBL:M60258; NID:g337766; PIDN:AAA36596.1; PI
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1991
A;Note: cerebroside sulfate activator protein mutant MU-6; corresponds to alternative sp
R;Kondoh, K.; Haneno, T.; Sano, A.; Kakimoto, Y.
Biochem. Biophys. Res. Commun. 181, 286-292, 1991
A;Title: Isolation and characterization of prosaposin from human milk.
A;Reference number: PS0330; MUID:92068206; PMID:1958198
A;Accession: PS0330
A;Molecule type: protein
A;Residues: 17-24,'X',26 <KON>
A;Cross-references: UNIPARC:UPI00001741B5
A;Experimental source: milk
R;Kretz, K.A.; Carson, G.S.; Morimoto, S.; Kishimoto, Y.; Fluharty, A.L.; O'Brien, J.S.
Proc. Natl. Acad. Sci. U.S.A. 87, 2541-2544, 1990
A;Title: Characterization of a mutation in a family with saposin B deficiency: a glycosy
A;Reference number: A35985; MUID:90207231; PMID:2320574
A;Accession: A35985
A;Molecule type: mRNA
A;Residues: 213-221 <KRE>
A;Cross-references: UNIPARC:UPI00001741B6; GB:M32221
A;Accession: B35985
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-259,263-527 <KR2>

A;Cross-references: UNIPARC:UPI00000000DBF; GB:M32221; NID:g337761; PIDN:AAA60303.1; PID:
A;Experimental source: lymphoblast
A;Accession: C35985
A;Molecule type: mRNA
A;Residues: 213-216,'I',218-221 <KR3>
A;Cross-references: UNIPARC:UPI00001741B7
A;Note: sequence from patients with activator-deficient metachromatic leukodystrophy; th
R;Fuerst, W.; Schubert, J.; Machleidt, W.; Meyer, H.E.; Sandhoff, K.
Eur. J. Biochem. 192, 709-714, 1990
A;Title: The complete amino-acid sequences of human ganglioside GM2 activator protein an
A;Reference number: S13195; MUID:91006165; PMID:2209618
A;Accession: S13196
A;Molecule type: protein
A;Residues: 195-259,263-277 <FUE>
A;Cross-references: UNIPARC:UPI00001741B8
R;Morimoto, S.; Martin, B.M.; Yamamoto, Y.; Kretz, K.A.; O'Brien, J.S.; Kishimoto, Y.
Proc. Natl. Acad. Sci. U.S.A. 86, 3389-3393, 1989
A;Title: Saposin A: second cerebroside activator protein.
A;Reference number: A32784; MUID:89240739; PMID:2717620
A;Accession: A32784
A;Molecule type: protein
A;Residues: 60-84;86-107;109-119;125-134 <MOR>
A;Cross-references: UNIPARC:UPI00001741B9; UNIPARC:UPI00001741BA; UNIPARC:UPI00001741BB;
R;O'Brien, J.S.; Kretz, K.A.; Dewji, N.; Wenger, D.A.; Esch, F.; Fluharty, A.L.
Science 241, 1098-1101, 1988
A;Title: Coding of two sphingolipid activator proteins (SAP-1 and SAP-2) by same genetic
A;Reference number: A41240; MUID:88321660; PMID:2842863
A;Accession: A41240
A;Molecule type: mRNA
A;Residues: 'GSSR',18-259,263-299,'D',301-302,'D',304-527 <OAB>
A;Cross-references: UNIPARC:UPI00001741BD; GB:J03086
R;Dewji, N.N.; Wenger, D.A.; O'Brien, J.S.
Proc. Natl. Acad. Sci. U.S.A. 84, 8652-8656, 1987
A;Title: Nucleotide sequence of cloned cDNA for human sphingolipid activator protein 1 f
A;Reference number: S02289; MUID:88068647; PMID:2825202
A;Accession: S02289
A;Status: significant sequence differences
A;Molecule type: mRNA
A;Cross-references: EMBL:J03015
A;Note: this sequence corrected by A41240
A;Note: part of this sequence, including the amino end of the mature protein, was determ
R;Kleinschmidt, T.; Christomanou, H.; Braunitzer, G.
Biol. Chem. Hoppe-Seyler 369, 1361-1365, 1988
A;Title: Complete amino-acid sequence of the naturally occurring A(2) activator protein
A;Reference number: S02028; MUID:89207118; PMID:3242555
A;Accession: S02028
A;Molecule type: protein
A;Residues: 195-259,263-276 <KLE>
A;Cross-references: UNIPARC:UPI00001741BE
R;Fuerst, W.; Machleidt, W.; Sandhoff, K.
Biol. Chem. Hoppe-Seyler 369, 317-328, 1988
A;Title: The precursor of sulfatide activator protein is processed to three different pr
A;Reference number: S00813; MUID:89000190; PMID:3048308
A;Accession: S00813
A;Molecule type: protein
A;Residues: 410-487 <FU2>
A;Cross-references: UNIPARC:UPI00001741BF
R;Kleinschmidt, T.; Christomanou, H.; Braunitzer, G.
Biol. Chem. Hoppe-Seyler 368, 1571-1578, 1987
A;Title: Complete amino-acid sequence and carbohydrate content of the naturally occurri
A;Reference number: S00226; MUID:88163077; PMID:3442600
A;Accession: S00226
A;Molecule type: protein
A;Residues: 314-393 <KL2>
A;Cross-references: UNIPARC:UPI000003ED8E
R;Vaccaro, A.M.; Salvati, R.; Barca, A.; Tatti, M.; Ciaffoni, F.; Maras, B.; Siciliano
J. Biol. Chem. 270, 9953-9960, 1995
A;Title: Structural analysis of saposin C and B. Complete localization of disulfide bri
A;Reference number: A57297; MUID:95247790; PMID:7730378
A;Contents: annotation; disulfide bonds; glycosylation
R;Holschmidt, H.; Sandhoff, K.; Fuerst, W.; Kwon, H.Y.; Schnabel, D.; Suzuki, K.
FEBS Lett. 280, 267-270, 1991
A;Title: The organization of the gene for the human cerebroside sulfate activator prote

A;Reference number: I37264; MUID:911192146; PMID:2013321

A;Accession: I37265

A;Status: translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 59-125 <RES>

A;Cross-references: UNIPARC:UPI000016A751; EMBL:X57107; NID:G30234; PIDN:CAA40391.1; PID

Query Match 100.0%; Score 412; DB 1; Length 527;

Best Local Similarity 100.0%; Pred. No. 5e-32;

Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SDVYCVCEFLVKEVTKLIDNNKTEKILDAFKMCKLPKSLSECCQEVVDYTGSSILS 60

|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 314 SDVYCVCEFLVKEVTKLIDNNKTEKILDAFKMCKLPKSLSECCQEVVDYTGSSILS 373

QY 61 ILLEEVSPVLVCSMLHLC 80

|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 374 ILLEEVSPVLVCSMLHLC 393

RESULT 2

S21770

saposin-C - bovine

C;Species: Bos primigenius taurus (cattle)

C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 31-Oct-1997

C;Accession: S21770

R;Sano, A.; Mizuno, T.; Kondoh, K.; Hinenno, T.; Ueno, S.; Kakimoto, Y.; Morita, N.

Biochim. Biophys. Acta 1120, 75-80, 1992

A;Title: Saposin-C from bovine spleen; complete amino acid sequence and relation between

A;Reference number: S21770; MUID:92207994; PMID:1554743

A;Accession: S21770

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-80 <SAN>

A;Cross-references: UNIPARC:UPI0000177939

C;Superfamily: saposin; saposin repeat homology

Query Match 83.3%; Score 343; DB 2; Length 80;

Best Local Similarity 79.7%; Pred. No. 3e-26;

Matches 63; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 1 SDVYCVCEFLVKEVTKLIDNNKTEKILDAFKMCKLPKSLSECCQEVVDYTGSSILS 60

:|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 1 ADYQCQCEFLVKEVTKLIDNNKTEKILDAFKMCKLPKSLSECCQEVVDYTGSSILS 60

QY 61 ILLEEVSPVLVCSMLHLC 79

|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 61 ILLEEVSPVLVCSMLHLC 79

RESULT 3

A32026

glucosylceramide beta-glucosidase activator protein SAP-2 - guinea pig

C;Species: Cavia porcellus (Guinea pig)

C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 09-Jul-2004

C;Accession: A32026

R;Sano, A.; Radin, N.S.; Johnson, L.L.; Tarr, G.E.

J. Biol. Chem. 263, 19597-19601, 1988

A;Title: The activator protein for glucosylceramide beta-glucosidase from guinea pig liv

A;Reference number: A32026; MUID:89066787; PMID:3198642

A;Accession: A32026

A;Molecule type: protein

A;Residues: 1-81 <SAN>

A;Cross-references: UNIPROT:P20097; UNIPARC:UPI000013555A

C;Superfamily: saposin; saposin repeat homology

F;1-81/Domain: saposin repeat homology <SAP>

Query Match 63.3%; Score 261; DB 2; Length 81;

Best Local Similarity 61.8%; Pred. No. 2.3e-18;

Matches 47; Conservative 18; Mismatches 11; Indels 0; Gaps 0;

QY 3 VYCEVCEFLVKEVTKLIDNNKTEKILDAFKMCKLPKSLSECCQEVVDYTGSSILS 62

|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 3 VTCKACEYVVKVMELIDNNRTEKIIHALDSVCALLPESVSEVCEVVDYTGDSIVALL 62

QY 63 LEEVSPVLVCSMLHLC 78

|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 63 LEEVSPVLVCSMLHLC 78

RESULT 4

A28716

saposin precursor - rat

N;Alternate names: cerabroside sulfate activator protein; co-beta-glucosidase; componen

ein (SAP); sphingolipid activator protein A2; sulfated glycoprotein 1; sulfatide sulfat

N;Contains: prosaposin; saposin A; saposin B; saposin C; saposin D

C;Species: Rattus norvegicus (Norway rat)

C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C;Accession: A28716

R;Collard, M.W.; Sylvester, S.R.; Tsuruta, J.K.; Griswold, M.D.

Biochemistry 27, 4557-4564, 1988

A;Title: Biosynthesis and molecular cloning of sulfated glycoprotein 1 secreted by rat

A;Reference number: A28716; MUID:89000647; PMID:3048385

A;Accession: A28716

A;Molecule type: mRNA

A;Residues: 1-554 <COL>

A;Cross-references: UNIPROT:P10960; UNIPARC:UPI000013555D; CB:M19936; NID:G206904; PIDN

A;Note: parts of this sequence, including the amino end of the mature protein, were det

C;Function:

A;Description: saposins bind sphingolipids, form hydrophilic complexes and make them ac

A;Pathway: sphingolipid catabolism

A;Note: saposins A and C (SAP-2) activate hydrolysis of glucocerebroside by beta-glucos-

A;Note: saposin B (SAP-1) activates hydrolysis of galactocerebroside sulfate by arylsul

A;Note: saposin D activates hydrolysis of sphingomyelin by sphingomyelin phosphodiester

C;Superfamily: saposin; saposin repeat homology

C;Keywords: alternative splicing; Glycoprotein; lysosomal storage disease; lysosome; sp;

F;1-16/Domain: signal sequence #status predicted <SIG>

F;17-554/Product: prosaposin #status predicted <PRO>

F;55-148/Domain: saposin repeat homology <SAP1>

F;60-143/Product: saposin A #status predicted <SAPA>

F;189-280/Domain: saposin repeat homology <SAP2>

F;194-273/Product: saposin B #status predicted <SAB1>

F;306-397/Domain: saposin repeat homology <SAP3>

F;310-389/Product: saposin C #status predicted <SAPC>

F;431-522/Domain: saposin repeat homology <SAP4>

F;437-514/Product: saposin D #status predicted <SAPD>

F;63-138,66-132,94-102,439-512,442-506,470-481/Diulfide bonds: #status predicted

F;80,214,331,456/Binding site: carbohydrate (Aen) (covalent) #status predicted

F;197-270,200-264,229-240,314-387,317-381,345-356/Diulfide bonds: #status predicted

Query Match 46.8%; Score 193; DB 1; Length 554;

Best Local Similarity 40.3%; Pred. No. 6.1e-11;

Matches 31; Conservative 24; Mismatches 22; Indels 0; Gaps 0;

QY 3 VYCEVCEFLVKEVTKLIDNNKTEKILDAFKMCKLPKSLSECCQEVVDYTGSSILS 62

|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 312 IFQVQVQLVKEVTKLIDNNKTEKILDAFKMCKLPKSLSECCQEVVDYTGSSILS 371

QY 63 LEEVSPVLVCSMLHLC 79

|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 372 MHEVNFPLCGVISLCS 388

RESULT 5

JH0604

saposin precursor - mouse

N;Alternate names: cerebroside sulfate activator protein; co-beta-glucosidase; componen

ein (SAP); sphingolipid activator protein A2; sulfated glycoprotein 1; sulfatide sulfat

N;Contains: prosaposin; saposin A; saposin B; saposin C; saposin D

C;Species: Mus musculus (house mouse)

C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C;Accession: JH0604

R;Tsuda, M.; Sakiyama, T.; Endo, H.; Kitagawa, T.

Biochem. Biophys. Res. Commun. 184, 1266-1272, 1992

A;Title: The primary structure of mouse saposin.

A;Reference number: JH0604; MUID:92272718; PMID:1590788

C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C;Accession: T48201
R;Bevan, M.; Peters, S.A.; van Staveren, M.; Dirkse, W.; Stiekema, W.; Bancroft, I.; Mew
submitted to the Protein Sequence Database, March 2000
A;Reference number: 224488
A;Accession: T48201
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-217 <BEV>
A;Cross-references: UNIPROT:Q9LZW6; UNIPARC:UPI000000A6022; EMBL:AL162351
A;Experimental source: cultivar Columbia; BAC clone T20L15
C;Genetics:
A;Map position: 5
A;Introns: 30/1; 79/3; 146/3; 166/3
A;Note: T20L15.70

Query Match 25.8%; Score 106.5; DB 2; Length 217;
Best Local Similarity 30.3%; Pred. No. 0.0048;
Matches 23; Conservative 20; Mismatches 32; Indels 1; Gaps 1;

QY 5 CEVCEFLVKEVTKLIDNNKTEKILDAFDKMCCKLPSLSECEQVVDVTYSSILSILLE 64
Db 126 CEACRETVEVVTYKDKPETKILIRLLKECKSL-NNYQDKCKMVFEGPLMLTDLOK 184

QY 65 EVSPELVCSMLHLC 80
Db 185 FLEKQDVCTILLHCPG 200

RESULT 8
T46069
hypothetical protein T18N14.110 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C;Accession: T46069
R;Deleany, M.; Berger, C.; Cooke, R.; Grellet, F.; Laudie, M.; Mewes, H.W.; Lemcke, K.;
submitted to the Protein Sequence Database, December 1999
A;Reference number: 223013
A;Accession: T46069
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-213
A;Cross-references: UNIPROT:Q9SCT5; UNIPARC:UPI000000AC273; EMBL:AL132968
A;Experimental source: cultivar Columbia; BAC clone T18N14
C;Genetics:
A;Map position: 3
A;Introns: 31/1; 80/3; 146/3; 166/3
A;Note: T18N14.110

Query Match 25.7%; Score 106; DB 2; Length 213;
Best Local Similarity 29.7%; Pred. No. 0.0052;
Matches 22; Conservative 16; Mismatches 34; Indels 2; Gaps 2;

QY 5 CEVCEFLVKEVTKLIDNNKTEKILDAFDKMCCKLPSLSECEQVVDVTYSSILSILLE 64
Db 40 CVLCEEYVDALSYLEKRVTAQELIEDLHRCSQL-RGVSQCISLVDYV-VPLFELQLE 97

QY 65 EVSPELVCSMLHLC 78
Db 98 SFQPHYFCKRMNLC 111

RESULT 9
S47096
cynarase (EC 3.4.23.-) - cardoon
C;Species: Cynara cardunculus (cardoon)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 29-Aug-1997
C;Accession: S47096
R;Cordeiro, M.C.; Xue, Z.T.; Pietrzak, M.; Pais, M.S.; Brodelius, P.
submitted to the EMBL Data Library, November 1992
A;Description: Tissue specific expression of cynarase (s) genes in flowers of Cynara ca.
A;Reference number: S47096
A;Accession: S47096

C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C;Accession: T48201
R;Bevan, M.; Peters, S.A.; van Staveren, M.; Dirkse, W.; Stiekema, W.; Bancroft, I.; Mew
submitted to the Protein Sequence Database, March 2000
A;Reference number: 224488
A;Accession: T48201
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-217 <BEV>
A;Cross-references: UNIPROT:Q9LZW6; UNIPARC:UPI000000A6022; EMBL:AL162351
A;Experimental source: cultivar Columbia; BAC clone T20L15
C;Genetics:
A;Map position: 5
A;Introns: 30/1; 79/3; 146/3; 166/3
A;Note: T20L15.70

Query Match 25.8%; Score 106.5; DB 2; Length 217;
Best Local Similarity 30.3%; Pred. No. 0.0048;
Matches 23; Conservative 20; Mismatches 32; Indels 1; Gaps 1;

QY 5 CEVCEFLVKEVTKLIDNNKTEKILDAFDKMCCKLPSLSECEQVVDVTYSSILSILLE 64
Db 126 CEACRETVEVVTYKDKPETKILIRLLKECKSL-NNYQDKCKMVFEGPLMLTDLOK 184

QY 65 EVSPELVCSMLHLC 80
Db 185 FLEKQDVCTILLHCPG 200

RESULT 8
T46069
hypothetical protein T18N14.110 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C;Accession: T46069
R;Deleany, M.; Berger, C.; Cooke, R.; Grellet, F.; Laudie, M.; Mewes, H.W.; Lemcke, K.;
submitted to the Protein Sequence Database, December 1999
A;Reference number: 223013
A;Accession: T46069
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-213
A;Cross-references: UNIPROT:Q9SCT5; UNIPARC:UPI000000AC273; EMBL:AL132968
A;Experimental source: cultivar Columbia; BAC clone T18N14
C;Genetics:
A;Map position: 3
A;Introns: 31/1; 80/3; 146/3; 166/3
A;Note: T18N14.110

Query Match 25.7%; Score 106; DB 2; Length 213;
Best Local Similarity 29.7%; Pred. No. 0.0052;
Matches 22; Conservative 16; Mismatches 34; Indels 2; Gaps 2;

QY 5 CEVCEFLVKEVTKLIDNNKTEKILDAFDKMCCKLPSLSECEQVVDVTYSSILSILLE 64
Db 40 CVLCEEYVDALSYLEKRVTAQELIEDLHRCSQL-RGVSQCISLVDYV-VPLFELQLE 97

QY 65 EVSPELVCSMLHLC 78
Db 98 SFQPHYFCKRMNLC 111

RESULT 9
S47096
cynarase (EC 3.4.23.-) - cardoon
C;Species: Cynara cardunculus (cardoon)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 29-Aug-1997
C;Accession: S47096
R;Cordeiro, M.C.; Xue, Z.T.; Pietrzak, M.; Pais, M.S.; Brodelius, P.
submitted to the EMBL Data Library, November 1992
A;Description: Tissue specific expression of cynarase (s) genes in flowers of Cynara ca.
A;Reference number: S47096
A;Accession: S47096

A;Status: preliminary
A:Molecule type: mRNA
A;Residues: 1-428 <COR>
C;Cross-references: UNIPARC:UPI0000175D80; EMBL:X69193
C;Comment: The pair of saposin repeat homology domains tagged SAP1 and SAP2 represent a C;Superfamily: oryzasin; saposin repeat homology
C;Keywords: aspartic proteinase; hydrolase
F;236-281/Domain: saposin repeat homology #status atypical <SAP1>
F;290-339/Domain: saposin repeat homology #status atypical <SAP2>
P;230,210/Active site: Asp #status predicted

Query Match 25.7%; Score 106; DB 2; Length 428;
Best Local Similarity 45.9%; Pred. No. 0.011;
Matches 17; Conservative 10; Mismatches 10; Indels 0; Gaps 0;

QY 43 LSECEQVVDVTGSSILSLLEEVSPVLGVCSMLHLCS 79
 ::: : ||| ::||| ::||| ::||| ::||
Db 236 MSQQCKSLVDVGKSMIELLSSEQPEKICKSQMKICS 272

RESULT 10
T12049
cyprosin (SC 3.4.23.-) - cardoon (fragment)
N;Alternate names: cynarase
C;Species: Cynara cardunculus (cardoon)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C;Accession: T12049
R;Cordeiro, M.C.; Xue, Z.T.; Pietrzak, M.; Pais, M.S.; Brodelius, P.E.
Plant Mol. Biol. 24, 733-741, 1994
A;Title: Isolation and characterization of a cDNA from flowers of Cynara cardunculus end
A;Reference number: Z17395; MUID:94250836; PMID:8193298
A;Accession: T12049
A;Status: preliminary; translated from GE/EMBL/DDBY
A:Molecule type: mRNA
A;Residues: 1-474 <COR>
A;Cross-references: UNIPARC:UPI000016E005; EMBL:X69193; NID:g499015; PIDN:CAR48939.1; PT
A;Experimental source: flower
C;Superfamily: oryzasin; saposin repeat homology
C;Keywords: aspartic proteinase; hydrolase

Query Match 25.7%; Score 106; DB 2; Length 474;
Best Local Similarity 45.9%; Pred. No. 0.012;
Matches 17; Conservative 10; Mismatches 10; Indels 0; Gaps 0;

QY 43 LSECEQVVDVTGSSILSLLEEVSPVLGVCSMLHLCS 79
 ::: : ||| ::||| ::||| ::||| ::||
Db 282 MSQQCKSLVDVGKSMIELLSSEQPEKICKSQMKICS 318

RESULT 11
F86253
hypothetical protein [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: F86253
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chen, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.P.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.;
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: F86253
A;Status: preliminary
A:Molecule type: DNA
A;Residues: 1-506 <STO>
A;Cross-references: UNIPROT:O65390; UNIPARC:UPI000000BD7C; GB:AEO05172; NID:g3157937; PT
C;Genetics:
A;Map position: 1

C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: E96649
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, G.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: E96649
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-433 <STO>
A;Cross-references: UNIPROT:Q04593; UNIPARC:UPI000016DA70; GB:AE005173; NID:G2160151; PI
C;Genetics:
A;Gene: F19K23.21
A;Map position: 1
C;Superfamily: oryzasin; saposin repeat homology

Query Match 25.0%; Score 103; DB 2; Length 433;
Best Local Similarity 45.9%; Pred. No. 0.021;
Matches 17; Conservative 10; Mismatches 10; Indels 0; Gaps 0;
QY 43 LSECEQVVDYTGSSILLESPELVCSMLHCS 79
DB 333 VSQCKTVVDYQGTILDLLAETQPKKICSGILCA 369

RESULT 15
S02766
pulmonary surfactant protein B precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 09-Jul-2004
C;Accession: S02766
R;Emrie, P.A.; Shannon, J.M.; Mason, R.J.; Fisher, J.H.
Biochim. Biophys. Acta 994, 215-221, 1989
A;Title: cDNA and deduced amino acid sequence for the rat hydrophobic pulmonary surfacta
A;Reference number: S02766; MUID:89150284; PMID:2920185
A;Accession: S02766
A;Molecule type: mRNA
A;Residues: 1-376 <EMR>
A;Cross-references: UNIPROT:P22355; UNIPARC:UPI00001327F8; EMBL:X14778; NID:G57284; PIDN
C;Superfamily: pulmonary surfactant protein B; saposin repeat homology
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-190/Domain: propeptide #status predicted <PRO>
F;159-151/Domain: saposin repeat homology <SAP1>
F;190-277/Domain: saposin repeat homology <SAP2>
F;191-269/Product: pulmonary surfactant protein B #status predicted <MAT>
F;286-371/Domain: saposin repeat homology <SAP3>

Query Match 24.9%; Score 102.5; DB 2; Length 376;
Best Local Similarity 28.0%; Pred. No. 0.021;
Matches 21; Conservative 18; Mismatches 35; Indels 1; Gaps 1;
QY 5 CEVCEFLVKEVTKLIDNNKTEKILDAFKMCKLP-KSLSECEQVVDYTGSSILSILL 63
DB 67 CQCEEDIVHLLTQWTKEDAFQDTIRKFLQECEDILPKLLVPRCQVLDVLPVLDYFQ 126
QY 64 EVVSEPLVCSMLHLC 78
DB 127 GQIKPRAICSHVGLC 141

Search completed: January 13, 2006, 16:35:20
Job time : 6.35762 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 13, 2006, 16:16:04 ; Search time 183.053 Seconds
(without alignments)
1257.748 Million cell updates/sec

Title: US-10-801-517-1
Perfect score: 2789
Sequence: 1 MYALFLASLLGALAGPVL.....NTETAQCNAVECHRRHVN 524

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq 21.*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003be:*
8: Geneseqp2004s:*
9: Geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2789	100.0	524	2 AAR70783	Aar70783 Prosaposin
2	2789	100.0	524	2 AAW5652	Aaw5652 Human pro
3	2789	100.0	524	3 AAY58716	Aay58716 Human pro
4	2789	100.0	524	6 ABU79099	Abu79099 Lip-TAA b
5	2789	100.0	524	6 ABU05200	Abu05200 Human exp
6	2789	100.0	524	6 ABU05207	Abu05207 Human exp
7	2789	100.0	524	6 ABU05203	Abu05203 Human exp
8	2789	100.0	524	6 ABU07340	Abu07340 Human exp
9	2789	100.0	524	6 ABU05216	Abu05216 Human exp
10	2789	100.0	524	6 ABU05202	Abu05202 Human exp
11	2789	100.0	524	6 ABU05214	Abu05214 Human exp
12	2789	100.0	524	6 ABU05215	Abu05215 Human exp
13	2789	100.0	524	6 ABU05199	Abu05199 Human exp
14	2789	100.0	524	6 ABU05212	Abu05212 Human exp
15	2789	100.0	524	6 ABU05213	Abu05213 Human exp
16	2789	100.0	524	6 ABU05205	Abu05205 Human exp
17	2789	100.0	524	7 ADP43340	Adp43340 Superanti
18	2789	100.0	524	7 ADJ69401	Adj69401 Human hea
19	2789	100.0	524	8 ADO08060	Ado08060 Human pol
20	2789	100.0	524	8 ADQ94328	Adq94328 Human Pre
21	2789	100.0	524	8 ABM61149	Abm61149 Tumour-as
22	2789	100.0	524	8 ADS87894	Ads87894 Human pro
23	2789	100.0	524	8 ADU48630	Adu48630 Human pro
24	2789	100.0	524	9 ADW80727	Adw80727 Human pro

25	2789	100.0	524	9 ADX06774	Adx06774 Cyclin-de
26	2789	100.0	524	9 ADY14302	Ady14302 PRO polyP
27	2779	99.6	524	6 ABU05208	Abu05208 Human exp
28	2777.5	99.6	527	4 AAB31915	Aab31915 Amino aci
29	2777.5	99.6	527	5 ABP68602	Abp68602 Human pan
30	2777.5	99.6	527	6 ABU79100	Abu79100 Lip-TAA b
31	2777.5	99.6	527	6 ABU05204	Abu05204 Human exp
32	2777.5	99.6	527	6 ABU05210	Abu05210 Human exp
33	2777.5	99.6	527	7 ADF43341	Adf43341 Superanti
34	2772.5	99.4	523	4 AAB31916	Aab31916 Amino aci
35	2772.5	99.4	523	6 ABU05211	Abu05211 Human exp
36	2768	99.2	526	6 ABU05209	Abu05209 Human exp
37	2767.5	99.2	527	6 ABU05206	Abu05206 Human exp
38	2731	97.9	522	8 ADU24090	Adu24090 Human cys
39	2449.5	87.8	479	6 ABR39442	AbR39442 Human GEN
40	2024.5	72.6	385	6 ABR41750	AbR41750 Human DIT
41	1969	70.6	554	7 ADB85295	AdB85295 Rat tubul
42	1921	68.9	554	5 ABB57102	Abb57102 Mouse isc
43	1293.5	46.4	268	8 ADF29875	AdF29875 Human sec
44	1201	43.1	507	8 ADS87898	AdS87898 Human hyp
45	1201	43.1	521	3 AAY56966	Aay56966 Human SBP

ALIGNMENTS

RESULT 1
AAR70783
ID AAR70783 standard; protein; 524 AA.
XX
AC AAR70783;
XX
DT 25-MAR-2003 (revised)
DT 30-AUG-1995 (first entry)
XX
DE Prosaposin.
XX
KW Saposin-C; neuron; myelination; nervous system; neuroblastoma;
KW neurotrophic peptide; multiple sclerosis; leukoencephalitis;
KW adrenal leukodystrophy; prosaposin.
XX
OS Homo sapiens.
XX
PN WO9503821-A1.
XX
PD 09-FEB-1995.
XX
PF 28-JUL-1994; 94WO-US008453.
XX
PR 30-JUL-1993; 93US-00100247.
PR 21-APR-1994; 94US-00232513.
XX
PA (OBRI/) O'BRIEN J S.
XX
PI O'brien JS, Kishimoto Y;
XX
DR WPI; 1995-082029/11.
DR N-PSDB; AAQ85355.
XX
PT Stimulating neural cell out-growth and myelination - with pro.saposin,
PT saposin C or new neurotrophic peptide(s) from cytokine(s), for treating
XX nervous system diseases.
XX
PS Disclosure; Page 30-32; 50pp; English.
XX
CC The peptide given in AAR70773, corresponding to amino acids 8-29 of human
CC saposin-C (AAR70784), promotes neurite outgrowth in vitro. A consensus
CC sequence was determined by comparing the peptide with hematopoietic and
CC neurotrophic cytokines, and neurotrophic peptides (AAR70774-82) were
CC identified in the AB loop of human ciliary neurotrophic factor,
CC interleukin-6, -2, -3 and -gamma, erythropoietin and leukocyte
CC inhibitory factor, and in helix C of human interleukin-1-beta and
CC oncostatin-M. Prosaponin (AAR70783) and saposin-C also promoted nerve

CC	cell myelination ex vivo. (Updated on 25-MAR-2003 to correct PN field.)
CC	(Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to
CC	correct PI field.)
XX	
XX	
SQ	Sequence 524 AA;
	Query Match 100.0%; Score 2789; DB 2; Length 524;
	Best Local Similarity 100.0%; Pred. No. 4.6e-237;
	Matches 524; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 MYALFLASLAGAALAGPVGLGKECTRGSAVWCQNVKTASDCGAVKHCLQTVWVKPTVKS 60
DB	1 MYALFLASLAGAALAGPVGLGKECTRGSAVWCQNVKTASDCGAVKHCLQTVWVKPTVKS 60
QY	61 LPDCICKDVVTAAGDMLKDNATEBEILVYLEKTCDWLPKPNMSASCKEIVDSYLPVILDI 120
DB	61 LPDCICKDVVTAAGDMLKDNATEBEILVYLEKTCDWLPKPNMSASCKEIVDSYLPVILDI 120
QY	121 IKGMSRPGEVCSALNLCESLQKHLAELNHQKLESNKI PELDMTEVVAPFMANIPLILY 180
DB	121 IKGMSRPGEVCSALNLCESLQKHLAELNHQKLESNKI PELDMTEVVAPFMANIPLILY 180
QY	181 PDGPRSKPQPKNDGVDQCDCIQMTVDIQTAVRTNSTFVQALVEHVKECDRLGPGMADI 240
DB	181 PDGPRSKPQPKNDGVDQCDCIQMTVDIQTAVRTNSTFVQALVEHVKECDRLGPGMADI 240
QY	241 CKNYISOYSEIATIQMMHMQPKEICALVGFCDVEKEMPQTLVPAKVASKNVIPALELVE 300
DB	241 CKNYISOYSEIATIQMMHMQPKEICALVGFCDVEKEMPQTLVPAKVASKNVIPALELVE 300
QY	301 PIKKEHVPAKSDVYCEVCEFLVKTVIDNNKTEKILDAFDKMKSLPSLSECEQV 360
DB	301 PIKKEHVPAKSDVYCEVCEFLVKTVIDNNKTEKILDAFDKMKSLPSLSECEQV 360
QY	361 VDTYSSLSILLESVPELVCSMLHLCSTGTPALTVHVTPQDKGGFCEVCKLGVGLD 420
DB	361 VDTYSSLSILLESVPELVCSMLHLCSTGTPALTVHVTPQDKGGFCEVCKLGVGLD 420
QY	421 RNLEKNSTQKEILAALEKCSFLPPYQKQCDQFVAEYEPVLEILVEVMPFSFYCLKIG 480
DB	421 RNLEKNSTQKEILAALEKCSFLPPYQKQCDQFVAEYEPVLEILVEVMPFSFYCLKIG 480
QY	481 ACPSAHKPLLTGTEKINGSPYWCQNTETAACNAVEHCKRHWVN 524
DB	481 ACPSAHKPLLTGTEKINGSPYWCQNTETAACNAVEHCKRHWVN 524
RESULT 2	
AAW85652	
ID	AAW85652 standard; protein; 524 AA.
AC	AAW85652;
XX	
XX	
DT	19-JUL-1999 (first entry)
XX	
DE	Human prosaposin N-terminal peptide.
XX	
KW	Prosaposin; saposin; prosaptides; prosaposin receptor agonists; PRA;
KW	peripheral nervous system; central nervous system; PNS; CNS; Akt; Bcl-2;
KW	therapy; treatment; apoptosis; caspase; tumour necrosis factor; TNF;
KW	cytokine; interferon gamma; IFN; inflammation; rheumatoid arthritis;
KW	Crohn's disease; irritable bowel syndrome; asthma; cardiac infarction;
KW	congestive heart failure; multiple sclerosis;
KW	acute disseminated inflammatory leukoencephalitis;
KW	progressive multifocal leukoencephalitis; Alzheimer's disease;
KW	Parkinson's disease; amyotrophic lateral sclerosis; Huntington's disease;
KW	ischemic heart disease; Guillain-Barre disease; alopecia; AIDS dementia;
KW	cerebral malaria; HTLV; neuropathy;
KW	inflammatory neurodegenerative disease; toxin-induced liver disease.
XX	
XX	Homo sapiens.
OS	
PN	W09912559-A1.

XX	
PD	
XX	18-MAR-1999.
PF	
XX	09-SEP-1998; 98WO-US019216.
XX	
PR	09-SEP-1997; 97US-0058352P.
XX	04-JUN-1998; 98US-0088129P.
XX	(REGC) UNIV CALIFORNIA.
PA	
XX	O'brien JS;
PI	
XX	WPI; 1999-229139/19.
DR	N-PSDB; AAX08488.
PT	
XX	Use of prosaposin receptor agonist.
PS	Claim 7; Fig 2; 90pp; English.
XX	
CC	Prosaposin is a 70kDa glycoprotein which is proteolytically processed to
CC	generate saposins A, B, C and D, all of which are similar to each other
CC	and have a similar placement of six cysteines, a glycosylation site and
CC	conserved proline residues. Prosaposin, saposin C and prosaposin derived
CC	peptides (prosaptides), have therapeutic applications in promoting
CC	recovery after toxic, traumatic, myocardial ishchaemic, degenerative and
CC	inherited lesions to the peripheral and central nervous system.
CC	Prosaposin receptor agonists (PRAs) inhibit proinflammatory cytokine-
CC	induced apoptosis by activation of the Ser/Thr protein kinase Akt. Akt
CC	disassociates complexes of Bcl-2 family members, such as BAD-Bcl-2,
CC	releasing Bcl-2 and its family members which inhibit caspases, thereby
CC	inhibiting apoptosis. An additional mechanism whereby PRAs inhibit
CC	apoptosis is by blocking activation of JNK, a proapoptotic signaling
CC	component. Within several minutes after binding to the receptor, PRAs
CC	block JNK activation induced by tumor necrosis factor-alpha (TNF alpha).
CC	The activation of JNK by TNF alpha is another well known mechanism for
CC	TNF alpha-induced, as well as other proinflammatory cytokine-induced
CC	apoptosis. The method can be used for inhibiting apoptosis which is
CC	caspase-mediated or induced by a proinflammatory cytokine, for example
CC	TNF alpha or interferon-gamma. It can be used for inhibiting apoptosis
CC	associated with a disorder such as e.g. rheumatoid arthritis, Crohn's
CC	disease, irritable bowel syndrome, asthma, cardiac infarction, congestive
CC	heart failure, multiple sclerosis, acute disseminated inflammatory
CC	leukoencephalitis, progressive multifocal leukoencephalitis, Alzheimer's
CC	disease, Parkinson's disease, amyotrophic lateral sclerosis, Huntington's
CC	disease, ischemic heart disease, Guillain-Barre disease, traumatic brain
CC	injury, traumatic spinal cord injury, alopecia, AIDS dementia, cerebral
CC	malaria, HTLV, neuropathy, inflammatory neurodegenerative disease, and
CC	toxin-induced liver disease. This 524 N-terminal peptide of prosaposin
CC	also acts as a prosaposin receptor agonist
XX	
SQ	Sequence 524 AA;
	Query Match 100.0%; Score 2789; DB 2; Length 524;
	Best Local Similarity 100.0%; Pred. No. 4.6e-237;
	Matches 524; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 MYALFLASLAGAALAGPVGLGKECTRGSAVWCQNVKTASDCGAVKHCLQTVWVKPTVKS 60
DB	1 MYALFLASLAGAALAGPVGLGKECTRGSAVWCQNVKTASDCGAVKHCLQTVWVKPTVKS 60
QY	61 LPDCICKDVVTAAGDMLKDNATEBEILVYLEKTCDWLPKPNMSASCKEIVDSYLPVILDI 120
DB	61 LPDCICKDVVTAAGDMLKDNATEBEILVYLEKTCDWLPKPNMSASCKEIVDSYLPVILDI 120
QY	121 IKGMSRPGEVCSALNLCESLQKHLAELNHQKLESNKI PELDMTEVVAPFMANIPLILY 180
DB	121 IKGMSRPGEVCSALNLCESLQKHLAELNHQKLESNKI PELDMTEVVAPFMANIPLILY 180
QY	181 PDGPRSKPQPKNDGVDQCDCIQMTVDIQTAVRTNSTFVQALVEHVKECDRLGPGMADI 240
DB	181 PDGPRSKPQPKNDGVDQCDCIQMTVDIQTAVRTNSTFVQALVEHVKECDRLGPGMADI 240
QY	241 CKNYISOYSEIATIQMMHMQPKEICALVGFCDVEKEMPQTLVPAKVASKNVIPALELVE 300

Db 241 CKNYISQYSEIAIQMMHMQPKEICALVGFCDVEMPMQTLVPAKVASKNVIPALELVE 300
QY 301 PIKKHEVPAKSDVYCEVCEFLVKEVTKLIDNNKTEKEILDADPKMCKSLPKSLSEBCEQV 360
Db 301 PIKKHEVPAKSDVYCEVCEFLVKEVTKLIDNNKTEKEILDADPKMCKSLPKSLSEBCEQV 360
QY 361 VDTYSSILSILLEEVSPELVCSMLHLCSTRLPALTVHTVTPKDGFCVCKKLVGYLD 420
Db 361 VDTYSSILSILLEEVSPELVCSMLHLCSTRLPALTVHTVTPKDGFCVCKKLVGYLD 420
QY 421 RNLEKKNSTQKEILAALEKGCFLPDPYQKQCDQFVAEYEPVLIEILVEVMDPSFVCLKIG 480
Db 421 RNLEKKNSTQKEILAALEKGCFLPDPYQKQCDQFVAEYEPVLIEILVEVMDPSFVCLKIG 480
QY 481 ACPSAHKPLLGTEKCIWGPSYWCNTETAACQNAVEHCKRHVWN 524
Db 481 ACPSAHKPLLGTEKCIWGPSYWCNTETAACQNAVEHCKRHVWN 524

RESULT 3

AAV58716 standard; protein; 524 AA.

AC AAV58716;

25-APR-2000 (first entry)

Human prosaposin.

Prosaposin; saponin B; antiangiogenic; angiogenesis inhibitor;

antitumour; antiproliferative; antimigratory; Kaposi's sarcoma; tumour;

human; therapy.

Homo sapiens.

Key Location/Qualifiers

Protein 195..275

Peptide /note= "mature saposin B"

Peptide /note= "specifically claimed antiangiogenic peptide of

Claim 23"

Peptide /note= "specifically claimed antiangiogenic peptide of

Claim 4"

WO200002902-A1.

20-JAN-2000.

12-JUL-1999; 99WO-US015772.

13-JUL-1998; 98US-0092647P.

(GILL/) GILL P S.

Gill PS;

WPI; 2000-171128/15.

Saposin B derived peptides, useful as inhibitors of angiogenesis and

tumor growth.

Disclosure; Page 18; 78pp; English.

The present sequence is that of human prosaposin, a precursor of saposin B. The invention is based on the discovery that saposin B, previously known to be involved in the hydrolysis of sphingolipids, has potent antiangiogenic and antitumour activity, and also has antiproliferative and antimigratory activity against endothelial cells. This activity is conserved in cryptic polypeptides as small as 5 amino acids (see AAV58684 -715), which can be synthetically prepared and used in vitro or in vivo for the treatment of undesired angiogenesis and tumor growth, especially

CC Kaposi's sarcoma (claimed). The polypeptides can also be used in conjunction with cytotoxic moieties to selectively kill certain cell types, e.g. for treatment of cancer, angiofibroma, neovascular glaucoma, arteriovenous malformation, nonunion fracture, arthritis and other connective tissue disorders, Osler-Weber syndrome, atherosclerotic plaque, psoriasis, corneal graft neovascularization, pyogenic granuloma, retrolental fibroplasia, diabetic retinopathy, scleroderma, haemangioma, trachoma, vascular adhesions and hypertrophic scars

XX Sequence 524 AA;

Query Match 100.0%; Score 2789; DB 3; Length 524;

Best Local Similarity 100.0%; Pred. No. 4.6e-237;

Matches 524; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYALFLLASLLGALAGPVGLKECTRGSAVVCQNVKTASDCGAVKHCLQTVNKKPTVKS 60

Db 1 MYALFLLASLLGALAGPVGLKECTRGSAVVCQNVKTASDCGAVKHCLQTVNKKPTVKS 60

QY 61 LFCDICQVYTAAGDMLKDNATEEELVYLEKTCDWLKPKNMSASCKEIVDSYLPVILDI 120

Db 61 LFCDICQVYTAAGDMLKDNATEEELVYLEKTCDWLKPKNMSASCKEIVDSYLPVILDI 120

QY 121 IKGEMSRPGEVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVVAFFMANIPLLLY 180

Db 121 IKGEMSRPGEVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVVAFFMANIPLLLY 180

QY 181 PDGGRSKPQKNDGVDVCCICQMTDICTAVRTNSTFVQALVEHVKEECDRILGPGWADI 240

Db 181 PDGGRSKPQKNDGVDVCCICQMTDICTAVRTNSTFVQALVEHVKEECDRILGPGWADI 240

QY 241 CKNYISQYSEIAIQMMHMQPKEICALVGFCDVEMPMQTLVPAKVASKNVIPALELVE 300

Db 241 CKNYISQYSEIAIQMMHMQPKEICALVGFCDVEMPMQTLVPAKVASKNVIPALELVE 300

QY 301 PIKKHEVPAKSDVYCEVCEFLVKEVTKLIDNNKTEKEILDADPKMCKSLPKSLSEBCEQV 360

Db 301 PIKKHEVPAKSDVYCEVCEFLVKEVTKLIDNNKTEKEILDADPKMCKSLPKSLSEBCEQV 360

QY 361 VDTYSSILSILLEEVSPELVCSMLHLCSTRLPALTVHTVTPKDGFCVCKKLVGYLD 420

Db 361 VDTYSSILSILLEEVSPELVCSMLHLCSTRLPALTVHTVTPKDGFCVCKKLVGYLD 420

QY 421 RNLEKKNSTQKEILAALEKGCFLPDPYQKQCDQFVAEYEPVLIEILVEVMDPSFVCLKIG 480

Db 421 RNLEKKNSTQKEILAALEKGCFLPDPYQKQCDQFVAEYEPVLIEILVEVMDPSFVCLKIG 480

QY 481 ACPSAHKPLLGTEKCIWGPSYWCNTETAACQNAVEHCKRHVWN 524

Db 481 ACPSAHKPLLGTEKCIWGPSYWCNTETAACQNAVEHCKRHVWN 524

RESULT 4

ABU79099

ID ABU79099 standard; protein; 524 AA.

XX AC ABU79099;

XX DT 18-JUN-2003 (first entry)

XX DE Lip-TAA binding protein, Prosaposin.

XX Superantigen; SAG; staphylococcal enterotoxin; tumour; cancer; apoptosis;

XX gene therapy; mammalian cell receptor; cytosolic;

XX tumour associated lipid; anergy; T cell; antigen presenting cell; APC;

XX tumouricidal immunocyte; antitumour.

XX Unidentified.

XX US2002177551-A1.

XX PD 28-NOV-2002.

XX

PF	30-MAY-2001; 2001US-00870759.	
XX	31-MAY-2000; 2000US-0208128P.	
XX	(TERM/) TERMAN D S.	
PA	Terman DS;	
PI	WPI; 2003-361759/34.	
XX		
DR	A mammalian cell receptor, useful in the treatment of cancer by binding	
PT	to tumor associated lipids where the binding induces anergy or apoptosis	
PT	in T cells and antigen presenting cells.	
XX	Disclosure; Page; 167pp; English.	
XX	The invention relates to a mammalian cell receptor, useful in the	
CC	treatment of cancer, which binds to tumor associated lipids and induces	
CC	anergy or apoptosis in the T cells and antigen presenting cells (APCs).	
CC	Also included are a mammalian cell useful in the treatment of cancer	
CC	where the receptor which binds tumor associated lipids and induces	
CC	cellular inactivation or death is deleted or functionally deactivated,	
CC	producing (M1) a tumouricidal immunocyte population in vivo in a mammal	
CC	(by allowing tumour associated lipids to contact immunocytes in which	
CC	receptors for immunosuppressive fatty acids, ceramides, glycolipids,	
CC	sphingolipids, glycosphingolipids, phosphosphingolipids, gangliosides,	
CC	sialylated glycans, lipopeptides and proteoglycolipids are inactivated or	
CC	deleted), a construct useful in the treatment of cancer comprising a	
CC	superantigen (SAG) nucleotide inserted into a virus, a mammalian T cell	
CC	useful in the treatment of cancer (where an adaptor protein which	
CC	inhibits T cell activation by tumour associated antigens is deleted or	
CC	functionally deactivated), a composition useful in the treatment of	
CC	cancer (comprising a lipid raft conjugated to a superantigen), producing	
CC	(M2) a tumouricidal immunocyte population ex vivo in a mammal (by	
CC	allowing tumour associated lipids to contact immunocytes, in which	
CC	receptors for the lipids are inactivated or deleted to produce a	
CC	tumouricidal immunocyte population, and administering the tumouricidally	
CC	activated immunocytes to the host), producing (M3) a tumouricidal APC	
CC	population ex vivo in a mammal (by allowing a tumour associated lipid to	
CC	contact APCs, in which receptors for the tumour associated lipids are	
CC	inactivated or deleted to produce a tumouricidally activated population,	
CC	and administering APCs to the host), producing a tumouricidal T cell	
CC	population ex vivo in a mammal) by allowing a tumour associated lipids to	
CC	contact T cells, in which adaptor proteins, which inhibit T cell	
CC	activation by tumour associated antigens, are deleted or functionally	
CC	deactivated to produce a tumouricidal population of T cells, and	
CC	administering the tumouricidally activated T cells to the host, or	
CC	allowing a superantigen-lipid raft to contact T cells ex vivo, and	
CC	administering the tumouricidally activated T cells to the host), treating	
CC	(M5) cancer in a mammal (by administering a lipid binding molecule which	
CC	binds immunosuppressive tumour associated lipids in vivo), producing (M6)	
CC	a tumouricidal T cell population in vivo in a mammal (by allowing a	
CC	tumour associated antigen to contact immunocytes in which adaptor	
CC	proteins which inhibit T cell activation by tumour associated antigens	
CC	are deleted or functionally deactivated) and producing (M7) a	
CC	tumouricidal T cell population ex vivo in a mammal comprising allowing a	
CC	superantigen-lipid raft conjugate to contact immunocytes in vivo. The	
CC	receptors, methods and compositions are useful for treating cancers and	
CC	tumours. Bacterial superantigens are co-administered or administered as	
CC	fusion constructs with anti-tumour proteins or motifs. The present	
CC	sequence represents a tumour antigen or a motif identifying a tumour	
CC	antigen, which can be functionally deactivated in the method of the	
CC	invention. Note: The sequence data for this patent did not form part of	
CC	the printed specification, but was obtained in electronic format from the	
CC	US patent office website at	
CC	"seqdata.uspto.gov/sequence.html?DocID=20020177551"	
XX	Sequence 524 AA;	
SQ		
Query Watch	100.0%; Score 2789; DB 6; Length 524;	
Best Local Similarity	100.0%; Pred. No. 4.6e-237;	
Matches 524; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	

XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
XX Example 2; SEQ ID NO 1866; 134pp; English.
XX
XX The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC lymphoma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 524 AA;

Query Match 100.0%; Score 2789; DB 6; Length 524;
Best Local Similarity 100.0%; Pred. No. 4.6e-237;
Matches 524; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYALFLLASLLGALAGPVLGLKECTRGSAVQNVKTSADCGAVKHCLQTVWVKPTVKS 60
Db 1 MYALFLLASLLGALAGPVLGLKECTRGSAVQNVKTSADCGAVKHCLQTVWVKPTVKS 60
QY 61 LPCDICKDVVTAAGDMLKONATBEEILVYLEKTCMDLPKPNMGSASCKEIVDSYLPVLIDI 120
Db 61 LPCDICKDVVTAAGDMLKONATBEEILVYLEKTCMDLPKPNMGSASCKEIVDSYLPVLIDI 120
QY 121 IKGEMSRPGVCSALNLCESLQKHLAELNHQKLESNKIPELDWTVEVAFPMANIPILLY 180
Db 121 IKGEMSRPGVCSALNLCESLQKHLAELNHQKLESNKIPELDWTVEVAFPMANIPILLY 180
QY 181 PQDGRSKPQKONGDVQCDCIQWTDIQTAVRTNSTFVQALVEHVKEECDRLPGGNADI 240
Db 181 PQDGRSKPQKONGDVQCDCIQWTDIQTAVRTNSTFVQALVEHVKEECDRLPGGNADI 240
QY 241 CKNYISOYSIAIQMMHMQPKEICLVGFCDEKEMPMOTLVPKAVSKNVIIPALELVE 300
Db 241 CKNYISOYSIAIQMMHMQPKEICLVGFCDEKEMPMOTLVPKAVSKNVIIPALELVE 300
QY 301 PIKKEHVPAKSDVYCEVCEFLVKEVTKLIDNNKTEKEILDAFDKMCCKLPSLSECEQV 360
Db 301 PIKKEHVPAKSDVYCEVCEFLVKEVTKLIDNNKTEKEILDAFDKMCCKLPSLSECEQV 360
QY 361 VDTYGSISILLSEVSPVLCVSMHLHCSGTRLPALTVHTVTPKDGSGFCEVCKLGVGLD 420
Db 361 VDTYGSISILLSEVSPVLCVSMHLHCSGTRLPALTVHTVTPKDGSGFCEVCKLGVGLD 420
QY 421 RNLEKNSTKQEILAALESKGSFLPDPYKQKCDQVAVSEVPEVLILVEVMDPSFVCLKIG 480
Db 421 RNLEKNSTKQEILAALESKGSFLPDPYKQKCDQVAVSEVPEVLILVEVMDPSFVCLKIG 480
QY 481 ACPSAHKPLLTGTEKICINGPSYWCQNTTETAACQNAVEHCKRHVN 524
Db 481 ACPSAHKPLLTGTEKICINGPSYWCQNTTETAACQNAVEHCKRHVN 524

RESULT 6
ABU05207
ID ABU05207 standard; protein; 524 AA.
XX

AC ABU05207;
XX 29-JAN-2003 (first entry)
DT Human expressed protein tag (EPT) #1873.
DE
XX
XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX Homo sapiens.
OS
XX WO200278524-A2.
PN
XX 10-OCT-2002.
PD
XX 28-MAR-2002; 2002WO-US009671.
PF
XX 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX (ZYCO-) ZYCOS INC.
PA
XX Chicz RM, Tomlinson AJ, Urban RG;
PI WPI; 2003-040607/03.
XX
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
XX Example 2; SEQ ID NO 1873; 134pp; English.
XX
XX The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 524 AA;

Query Match 100.0%; Score 2789; DB 6; Length 524;
Best Local Similarity 100.0%; Pred. No. 4.6e-237;
Matches 524; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYALFLLASLLGALAGPVLGLKECTRGSAVQNVKTSADCGAVKHCLQTVWVKPTVKS 60
Db 1 MYALFLLASLLGALAGPVLGLKECTRGSAVQNVKTSADCGAVKHCLQTVWVKPTVKS 60
QY 61 LPCDICKDVVTAAGDMLKONATBEEILVYLEKTCMDLPKPNMGSASCKEIVDSYLPVLIDI 120
Db 61 LPCDICKDVVTAAGDMLKONATBEEILVYLEKTCMDLPKPNMGSASCKEIVDSYLPVLIDI 120
QY 121 IKGEMSRPGVCSALNLCESLQKHLAELNHQKLESNKIPELDWTVEVAFPMANIPILLY 180

Db 121 IKGEMSRPGEVCSALNLCESLQKHLAEHLNHQKLESNKIPELDMTEVVAPFMANIPLLLY 180
QY 181 PDGPRSKPQPKNDGVDQCDCIQMVTDIQTAVRTNSTFVQALVEHVKEECDRLGFGMADI 240
Db 181 PDGPRSKPQPKNDGVDQCDCIQMVTDIQTAVRTNSTFVQALVEHVKEECDRLGFGMADI 240
QY 241 CKNYISQYSEIAIQMMHMQPKIEICALVGFCDVEKEMPQTLVPAKVASKNVIPALELVE 300
Db 241 CKNYISQYSEIAIQMMHMQPKIEICALVGFCDVEKEMPQTLVPAKVASKNVIPALELVE 300
QY 301 PIKKEHVPKSDVYCEVCEFLVKEVTKLIDNNKTEKELIDAFDMCKSLPKSLSECEQEV 360
Db 301 PIKKEHVPKSDVYCEVCEFLVKEVTKLIDNNKTEKELIDAFDMCKSLPKSLSECEQEV 360
QY 361 VDTYSSSILSILLBEVSPVCSMLHLCSGTGLPALTVHVTPQKDGGEVCKKLVGYLD 420
Db 361 VDTYSSSILSILLBEVSPVCSMLHLCSGTGLPALTVHVTPQKDGGEVCKKLVGYLD 420
QY 421 RNLEKNSTKQETILAALEKGCSPFLDPYQKQCDQFVAEYEPVLIIEILVEVMDPSFVCLKIG 480
Db 421 RNLEKNSTKQETILAALEKGCSPFLDPYQKQCDQFVAEYEPVLIIEILVEVMDPSFVCLKIG 480
QY 481 ACPSAHKPLLTGTEKICWGPSYWCQNTETAAQNAVEHCKRHVMN 524
Db 481 ACPSAHKPLLTGTEKICWGPSYWCQNTETAAQNAVEHCKRHVMN 524

RESULT 7

ABU05203
ID ABU05203 standard; protein; 524 AA.

AC ABU05203;

XX 29-JAN-2003 (first entry)

XX Human expressed protein tag (EPT) #1869.

XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.

XX Homo sapiens.

XX WO2002/78524-A2.

XX 10-OCT-2002.

XX 28-MAR-2002; 2002WO-US009671.

XX 28-MAR-2001; 2001US-0279495P.

XX 21-MAY-2001; 2001US-0292544P.

XX 08-AUG-2001; 2001US-0310801P.

XX 01-OCT-2001; 2001US-0326370P.

XX 04-DEC-2001; 2001US-0336780P.

XX 20-FEB-2002; 2002US-0358985P.

XX (ZYCO-) ZYCOS INC.

XX Chicx RM, Tomlinson AJ, Urban RG;

XX WPI; 2003-040607/03.

XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.

XX Example 2; SEQ ID NO 1869; 134pp; English.

XX The invention describes a purified polypeptide, which comprises a

CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 524 AA;

Query Match 100.0%; Score 2789; DB 6; Length 524;

Best Local Similarity 100.0%; Pred. No. 4.6e-237;

Matches 524; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYALFLLASLLGAALAGPVLGLKECTRGSAVWCQNVKTASDCGAVKHCLQTVWNKPTVKS 60

Db 1 MYALFLLASLLGAALAGPVLGLKECTRGSAVWCQNVKTASDCGAVKHCLQTVWNKPTVKS 60

QY 61 LPDCICKDVVTAAGDMLKDNATEBEILVYLEKTCDWLPKPNMSASCKEIVDSYLPVILDI 120

Db 61 LPDCICKDVVTAAGDMLKDNATEBEILVYLEKTCDWLPKPNMSASCKEIVDSYLPVILDI 120

QY 121 IKGEMSRPGEVCSALNLCESLQKHLAEHLNHQKLESNKIPELDMTEVVAPFMANIPLLLY 180

Db 121 IKGEMSRPGEVCSALNLCESLQKHLAEHLNHQKLESNKIPELDMTEVVAPFMANIPLLLY 180

QY 181 PDGPRSKPQPKNDGVDQCDCIQMVTDIQTAVRTNSTFVQALVEHVKEECDRLGFGMADI 240

Db 181 PDGPRSKPQPKNDGVDQCDCIQMVTDIQTAVRTNSTFVQALVEHVKEECDRLGFGMADI 240

QY 241 CKNYISQYSEIAIQMMHMQPKIEICALVGFCDVEKEMPQTLVPAKVASKNVIPALELVE 300

Db 241 CKNYISQYSEIAIQMMHMQPKIEICALVGFCDVEKEMPQTLVPAKVASKNVIPALELVE 300

QY 301 PIKKEHVPKSDVYCEVCEFLVKEVTKLIDNNKTEKELIDAFDMCKSLPKSLSECEQEV 360

Db 301 PIKKEHVPKSDVYCEVCEFLVKEVTKLIDNNKTEKELIDAFDMCKSLPKSLSECEQEV 360

QY 361 VDTYSSSILSILLBEVSPVCSMLHLCSGTGLPALTVHVTPQKDGGEVCKKLVGYLD 420

Db 361 VDTYSSSILSILLBEVSPVCSMLHLCSGTGLPALTVHVTPQKDGGEVCKKLVGYLD 420

QY 421 RNLEKNSTKQETILAALEKGCSPFLDPYQKQCDQFVAEYEPVLIIEILVEVMDPSFVCLKIG 480

Db 421 RNLEKNSTKQETILAALEKGCSPFLDPYQKQCDQFVAEYEPVLIIEILVEVMDPSFVCLKIG 480

QY 481 ACPSAHKPLLTGTEKICWGPSYWCQNTETAAQNAVEHCKRHVMN 524

Db 481 ACPSAHKPLLTGTEKICWGPSYWCQNTETAAQNAVEHCKRHVMN 524

RESULT 8

ABU07340

ID ABU07340 standard; protein; 524 AA.

XX AC ABU07340;

XX 29-JAN-2003 (first entry)

XX Human expressed protein tag (EPT) #2041.

XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;

KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
 XX adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.

OS Homo sapiens.

PN WO200278524-A2.

PD 10-OCT-2002.

XX 28-MAR-2002; 2002WO-US009671.

XX 28-MAR-2001; 2001US-0279495P.

PR 21-MAY-2001; 2001US-0292544P.

PR 08-AUG-2001; 2001US-0310801P.

PR 01-OCT-2001; 2001US-0326370P.

PR 04-DEC-2001; 2001US-0336780P.

PR 20-FEB-2002; 2002US-0358985P.

XX (ZYCO-) ZYCOS INC.

XX Chicx RM, Tomlinson AJ, Urban RG;

XX WPI; 2003-040607/03.

XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
 XX cytoskeletal proteins, receptors or transcription factors), useful for
 XX treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
 XX leukemia.

XX Example 2: SEQ ID NO 2041; 134pp; English.

XX The invention describes a purified polypeptide, which comprises a
 XX fragment of a kinase, phosphatase, protease, protease inhibitor,
 XX transporter, cytoskeletal protein, receptor or transcription factor. The
 XX polypeptide is useful as an immunogenic composition for eliciting in a
 XX mammal an immunogenic response directed against any of the purified
 XX polypeptide. The purified polypeptide, or the antibody that binds to this
 XX polypeptide, is useful for treating cancer. The polypeptide is also
 XX useful for identifying compounds that binds to a naturally processed
 XX class I or class II MHC-binding polypeptide. The polypeptides and
 XX polynucleotides are particularly useful for treating or preventing
 XX myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
 XX lymphoma or leukaemia. These are also useful for screening agents for
 XX treating the above mentioned diseases. This sequence represents an
 XX expressed protein tag (EPT) isolated from human tissue for translational
 XX profiling. Note: This sequence does not appear in the printed
 XX specification but was obtained in electronic format directly from WIPO at
 XX ftp.wipo.int/pub/published_pct_sequences

XX Sequence 524 AA;

Query Match 100.0%; Score 2789; DB 6; Length 524;
 Best Local Similarity 100.0%; Pred. No. 4.6e-237;
 Matches 524; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MYALFLASLIGALAGPVLGLKECTRGSAVQNVKTA	SDCCGAVKHCLQTVWVKPTVKS	60
DB	1	MYALFLASLIGALAGPVLGLKECTRGSAVQNVKTA	SDCCGAVKHCLQTVWVKPTVKS	60
QY	61	LPDCIDKDVVTAAGDMLKONATEEEILVLEKTC	DWLPKPNMSASCKEIVDSYLPVLDI	120
DB	61	LPDCIDKDVVTAAGDMLKONATEEEILVLEKTC	DWLPKPNMSASCKEIVDSYLPVLDI	120
QY	121	IKGEMSRPGVCSALNLCESLQKHLAEINHQLES	NIPELDMTEVAVPFMANIPILLY	180
DB	121	IKGEMSRPGVCSALNLCESLQKHLAEINHQLES	NIPELDMTEVAVPFMANIPILLY	180
QY	181	PQDGRSKPQKNGDVCDQCIQWVTDIQFAVRTN	STFVALVHVKEECDRIGPGWADI	240
DB	181	PQDGRSKPQKNGDVCDQCIQWVTDIQFAVRTN	STFVALVHVKEECDRIGPGWADI	240
QY	241	CKNYISQYSIAIQMMHMQPKIEICALVGFCDV	KEMPMTLVPKAVSKNVI PALELVE	300

Db	241	CKNYISQYSIAIQMMHMQPKIEICALVGFCDV	KEMPMTLVPKAVSKNVI PALELVE	300
QY	301	PIKKHEVPAKSDVYCEVCFVLVKEVTKLIDNN	KTKEILDAFDKMCCKLPKSLSECCQV	360
Db	301	PIKKHEVPAKSDVYCEVCFVLVKEVTKLIDNN	KTKEILDAFDKMCCKLPKSLSECCQV	360
QY	361	VDTYGSSILSILLEVSPVLCVSMHLCSGTLP	ALTVHVTQPKDGGPCVCKLVGYLD	420
Db	361	VDTYGSSILSILLEVSPVLCVSMHLCSGTLP	ALTVHVTQPKDGGPCVCKLVGYLD	420
QY	421	RNLEKNSTKQETLAALKEGCSFLPDPYOKQ	CDQFVAEYEPVLEILVEVMDPSFVCLKIG	480
Db	421	RNLEKNSTKQETLAALKEGCSFLPDPYOKQ	CDQFVAEYEPVLEILVEVMDPSFVCLKIG	480
QY	481	ACPSAHKPLLGTKEKCIWGPSYWCQNTETA	AQAQNAVEHCCKRHYWN	524
Db	481	ACPSAHKPLLGTKEKCIWGPSYWCQNTETA	AQAQNAVEHCCKRHYWN	524

RESULT 9

ABU05216

ID ABU05216 standard; protein; 524 AA.

XX AC ABU05216;

XX 29-JAN-2003 (first entry)

XX Human expressed protein tag (EPT) #1882.

XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
 KW protease; protease inhibitor; transporter; cytoskeletal protein;
 KW receptor; transcription factor; cancer; MHC;
 KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
 KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.

XX Homo sapiens.

XX WO200278524-A2.

XX 10-OCT-2002.

XX 28-MAR-2002; 2002WO-US009671.

XX 28-MAR-2001; 2001US-0279495P.

XX 21-MAY-2001; 2001US-0292544P.

XX 08-AUG-2001; 2001US-0310801P.

XX 01-OCT-2001; 2001US-0326370P.

XX 04-DEC-2001; 2001US-0336780P.

XX 20-FEB-2002; 2002US-0358985P.

XX (ZYCO-) ZYCOS INC.

XX Chicx RM, Tomlinson AJ, Urban RG;

XX WPI; 2003-040607/03.

XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
 XX cytoskeletal proteins, receptors or transcription factors), useful for
 XX treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
 XX leukemia.

XX Example 2: SEQ ID NO 1882; 134pp; English.

XX The invention describes a purified polypeptide, which comprises a
 XX fragment of a kinase, phosphatase, protease, protease inhibitor,
 XX transporter, cytoskeletal protein, receptor or transcription factor. The
 XX polypeptide is useful as an immunogenic composition for eliciting in a
 XX mammal an immunogenic response directed against any of the purified
 XX polypeptide. The purified polypeptide, or the antibody that binds to this
 XX polypeptide, is useful for treating cancer. The polypeptide is also
 XX useful for identifying compounds that binds to a naturally processed
 XX class I or class II MHC-binding polypeptide. The polypeptides and
 XX polynucleotides are particularly useful for treating or preventing

```
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 524 AA;

Query Match 100.0%; Score 2789; DB 6; Length 524;
Best Local Similarity 100.0%; Pred. No. 4.6e-237; Indels 0; Gaps 0;
Matches 524; Conservative 0; Mismatches 0;

QY 1 MYALFLLASLGAALAGVGLGKECTRGSAVWCQNVKTASDCGAVKHCLQTVWNKPTVKS 60
Db 1 MYALFLLASLGAALAGVGLGKECTRGSAVWCQNVKTASDCGAVKHCLQTVWNKPTVKS 60
QY 61 LPCDICKDVVTAAGDMLKDNATEBEILVYLEKTCDWLPKPNMSASCKEIVDSYLPVILI 120
Db 61 LPCDICKDVVTAAGDMLKDNATEBEILVYLEKTCDWLPKPNMSASCKEIVDSYLPVILI 120
QY 121 IKGMSRPGVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVVAPFMANIPLILY 180
Db 121 IKGMSRPGVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVVAPFMANIPLILY 180
QY 181 PQDGRSPKQPKDNGDVQCDCIQWVTDIQTAVRTNSTFVQALVEHVKECDRLGFGMADI 240
Db 181 PQDGRSPKQPKDNGDVQCDCIQWVTDIQTAVRTNSTFVQALVEHVKECDRLGFGMADI 240
QY 241 CKNYISQYSEIAIQMMHMQPKEICALVGFCDVEKEMPQTLVPAKVASKNVIPALELVE 300
Db 241 CKNYISQYSEIAIQMMHMQPKEICALVGFCDVEKEMPQTLVPAKVASKNVIPALELVE 300
QY 301 PIKKEVPAKSDVYCEVCEFLVKEVTKLIDNNKTEKILTDAFDKWCCKLPKSLSECCQEV 360
Db 301 PIKKEVPAKSDVYCEVCEFLVKEVTKLIDNNKTEKILTDAFDKWCCKLPKSLSECCQEV 360
QY 361 VDTYSSILSILLEVSPVLCVSMHLCSGTRLPALTVAHVTPQKDGGFCEVCKLVGYLD 420
Db 361 VDTYSSILSILLEVSPVLCVSMHLCSGTRLPALTVAHVTPQKDGGFCEVCKLVGYLD 420
QY 421 RNLEKNSTKQETLAALAKGCSFLPDYQKQCDQFVAEYEPVLIEILVEVMDPSFVCLKIG 480
Db 421 RNLEKNSTKQETLAALAKGCSFLPDYQKQCDQFVAEYEPVLIEILVEVMDPSFVCLKIG 480
QY 481 ACPSAHKPLLGTEKCIWGPSYWCQNTETAACQNAVEHCKRHVYN 524
Db 481 ACPSAHKPLLGTEKCIWGPSYWCQNTETAACQNAVEHCKRHVYN 524

RESULT 10
ABU05202
ID ABU05202 standard; protein; 524 AA.
AC
XX ABU05202;
XX
XX 29-JAN-2003 (first entry)
XX
XX Human expressed protein tag (EPT) #1868.
XX
XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
XX protease; protease inhibitor; transporter; cytoskeletal protein;
XX receptor; transcription factor; cancer; MHC;
XX major histocompatibility complex; myeloma; colon cancer; gastric cancer;
XX adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
XX Homo sapiens.
XX
XX WO200278524-A2.
XX
XX 10-OCT-2002.
```

```
PF 28-MAR-2002; 2002WO-US009671.
XX
XX 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX
XX (ZYCO-) ZYCOS INC.
XX
XX Chicx RM, Tomlinson AJ, Urban RG;
XX WPI; 2003-040607/03.
XX
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
XX cytoskeletal proteins, receptors or transcription factors), useful for
XX treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
XX leukemia.
XX
XX Example 2; SEQ ID NO 1868; 134pp; English.
XX
XX The invention describes a purified polypeptide, which comprises a
XX fragment of a kinase, phosphatase, protease, protease inhibitor,
XX transporter, cytoskeletal protein, receptor or transcription factor. The
XX polypeptide is useful as an immunogenic composition for eliciting in a
XX mammal an immunogenic response directed against any of the purified
XX polypeptide. The purified polypeptide, or the antibody that binds to this
XX polypeptide, is useful for treating cancer. The polypeptide is also
XX useful for identifying compounds that binds to a naturally processed
XX class I or class II MHC-binding polypeptide. The polypeptides and
XX polynucleotides are particularly useful for treating or preventing
XX myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
XX lymphoma or leukaemia. These are also useful for screening agents for
XX treating the above mentioned diseases. This sequence represents an
XX expressed protein tag (EPT) isolated from human tissue for translational
XX profiling. Note: This sequence does not appear in the printed
XX specification but was obtained in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 524 AA;

Query Match 100.0%; Score 2789; DB 6; Length 524;
Best Local Similarity 100.0%; Pred. No. 4.6e-237; Indels 0; Gaps 0;
Matches 524; Conservative 0; Mismatches 0;

QY 1 MYALFLLASLGAALAGVGLGKECTRGSAVWCQNVKTASDCGAVKHCLQTVWNKPTVKS 60
Db 1 MYALFLLASLGAALAGVGLGKECTRGSAVWCQNVKTASDCGAVKHCLQTVWNKPTVKS 60
QY 61 LPCDICKDVVTAAGDMLKDNATEBEILVYLEKTCDWLPKPNMSASCKEIVDSYLPVILI 120
Db 61 LPCDICKDVVTAAGDMLKDNATEBEILVYLEKTCDWLPKPNMSASCKEIVDSYLPVILI 120
QY 121 IKGMSRPGVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVVAPFMANIPLILY 180
Db 121 IKGMSRPGVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVVAPFMANIPLILY 180
QY 181 PQDGRSPKQPKDNGDVQCDCIQWVTDIQTAVRTNSTFVQALVEHVKECDRLGFGMADI 240
Db 181 PQDGRSPKQPKDNGDVQCDCIQWVTDIQTAVRTNSTFVQALVEHVKECDRLGFGMADI 240
QY 241 CKNYISQYSEIAIQMMHMQPKEICALVGFCDVEKEMPQTLVPAKVASKNVIPALELVE 300
Db 241 CKNYISQYSEIAIQMMHMQPKEICALVGFCDVEKEMPQTLVPAKVASKNVIPALELVE 300
QY 301 PIKKEVPAKSDVYCEVCEFLVKEVTKLIDNNKTEKILTDAFDKWCCKLPKSLSECCQEV 360
Db 301 PIKKEVPAKSDVYCEVCEFLVKEVTKLIDNNKTEKILTDAFDKWCCKLPKSLSECCQEV 360
QY 361 VDTYSSILSILLEVSPVLCVSMHLCSGTRLPALTVAHVTPQKDGGFCEVCKLVGYLD 420
Db 361 VDTYSSILSILLEVSPVLCVSMHLCSGTRLPALTVAHVTPQKDGGFCEVCKLVGYLD 420
```

QY 421 RNLEKNSTKQETLAALAEKGCSEFLPDYQKQCDQFVAEYEPVLIEILVEVMDPSFVCLKIG 480
 Db |||||||
 QY 421 RNLEKNSTKQETLAALAEKGCSEFLPDYQKQCDQFVAEYEPVLIEILVEVMDPSFVCLKIG 480
 Db |||||||
 QY 481 ACPSAHKPLLGTEKCIWGSPSYWQNTTETAACNAVEHCRRHVN 524
 Db |||||||
 QY 481 ACPSAHKPLLGTEKCIWGSPSYWQNTTETAACNAVEHCRRHVN 524
 Db |||||||

RESULT 11

ABU05214
 ID ABU05214 standard; protein; 524 AA.

XX AC ABU05214;

XX DT 29-JAN-2003 (first entry)

XX DE Human expressed protein tag (EPT) #1880.

XX KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
 KW protease; protease inhibitor; transporter; cytoskeletal protein;
 KW receptor; transcription factor; cancer; MHC;
 KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
 KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.

XX OS Homo sapiens.

XX PN WO200278524-A2.

XX PD 10-OCT-2002.

XX PF 28-MAR-2002; 2002WO-US009671.

XX PR 28-MAR-2001; 2001US-0279495P.

XX PR 21-MAY-2001; 2001US-0292544P.

XX PR 08-AUG-2001; 2001US-0310801P.

XX PR 01-OCT-2001; 2001US-0326370P.

XX PR 04-DEC-2001; 2001US-0336780P.

XX PR 20-FEB-2002; 2002US-0358985P.

XX PA (ZYCO-) ZYCOS INC.

XX PI Chiciz RM, Tomlinson AJ, Urban RG;

XX DR WPI; 2003-040607/03.

XX PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
 PT cytoskeletal proteins, receptors or transcription factors), useful for
 PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
 PT leukemia.

XX PS Example 2; SEQ ID NO 1880; 134pp; English.

XX CC The invention describes a purified polypeptide, which comprises a
 CC fragment of a kinase, phosphatase, protease, protease inhibitor,
 CC transporter, cytoskeletal protein, receptor or transcription factor. The
 CC polypeptide is useful as an immunogenic composition for eliciting in a
 CC mammal an immunogenic response directed against any of the purified
 CC polypeptide. The purified polypeptide, or the antibody that binds to this
 CC polypeptide, is useful for treating cancer. The polypeptide is also
 CC useful for identifying compounds that binds to a naturally processed
 CC class I or class II MHC-binding polypeptide. The polypeptides and
 CC polynucleotides are particularly useful for treating or preventing
 CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
 CC lymphoma or leukaemia. These are also useful for screening agents for
 CC treating the above mentioned diseases. This sequence represents an
 CC expressed protein tag (EPT) isolated from human tissue for translational
 CC profiling. Note: This sequence does not appear in the printed
 CC specification but was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 524 AA;

Query Match 100.0%; Score 2789; DB 6; Length 524;
 Best Local Similarity 100.0%; Pred. No. 4.6e-237;
 Matches 524; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYALFLASLIGALAGPVLGKECTRGSAVWCQVKTASDCGAVKHCLQTVNNKPTVKS 60
 Db |||||||
 QY 1 MYALFLASLIGALAGPVLGKECTRGSAVWCQVKTASDCGAVKHCLQTVNNKPTVKS 60
 Db |||||||
 QY 61 LPDCICKDVVTAAGDMLKDNATEEILVLEKTCDWLPKPNMSASCKEIVDSYLPVILI 120
 Db |||||||
 QY 61 LPDCICKDVVTAAGDMLKDNATEEILVLEKTCDWLPKPNMSASCKEIVDSYLPVILI 120
 Db |||||||
 QY 121 IKGEMSRFGEVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVVAFFMANIPLLY 180
 Db |||||||
 QY 121 IKGEMSRFGEVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVVAFFMANIPLLY 180
 Db |||||||
 QY 181 PQDGPRSRKQPKDNGDVQCDCIQMTVDIQTAVRTNSTFVQALVEHVKECDRLGPGWADI 240
 Db |||||||
 QY 181 PQDGPRSRKQPKDNGDVQCDCIQMTVDIQTAVRTNSTFVQALVEHVKECDRLGPGWADI 240
 Db |||||||
 QY 241 KKNYISQYSEIAIQMMHMQPKIEICALVGFCDVEKEMPMQTLVPAKVASKNVIPALELVE 300
 Db |||||||
 QY 241 KKNYISQYSEIAIQMMHMQPKIEICALVGFCDVEKEMPMQTLVPAKVASKNVIPALELVE 300
 Db |||||||
 QY 301 PIKKEHVPKSDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDKWCSEKLPKLSLSECBQV 360
 Db |||||||
 QY 301 PIKKEHVPKSDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDKWCSEKLPKLSLSECBQV 360
 Db |||||||
 QY 361 VDTYSSILSILLBEVSPBELVCSMLHLCSTGTRLPALTAVHTQPKDGGFCVCKLVGYLD 420
 Db |||||||
 QY 361 VDTYSSILSILLBEVSPBELVCSMLHLCSTGTRLPALTAVHTQPKDGGFCVCKLVGYLD 420
 Db |||||||
 QY 421 RNLEKNSTKQETLAALAEKGCSEFLPDYQKQCDQFVAEYEPVLIEILVEVMDPSFVCLKIG 480
 Db |||||||
 QY 421 RNLEKNSTKQETLAALAEKGCSEFLPDYQKQCDQFVAEYEPVLIEILVEVMDPSFVCLKIG 480
 Db |||||||
 QY 481 ACPSAHKPLLGTEKCIWGSPSYWQNTTETAACNAVEHCRRHVN 524
 Db |||||||
 QY 481 ACPSAHKPLLGTEKCIWGSPSYWQNTTETAACNAVEHCRRHVN 524
 Db |||||||

RESULT 12

ABU05215

ID ABU05215 standard; protein; 524 AA.

XX AC ABU05215;

XX DT 29-JAN-2003 (first entry)

XX DE Human expressed protein tag (EPT) #1881.

XX KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
 KW protease; protease inhibitor; transporter; cytoskeletal protein;
 KW receptor; transcription factor; cancer; MHC;
 KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
 KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.

XX OS Homo sapiens.

XX PN WO200278524-A2.

XX PD 10-OCT-2002.

XX PF 28-MAR-2002; 2002WO-US009671.

XX PR 28-MAR-2001; 2001US-0279495P.

XX PR 21-MAY-2001; 2001US-0292544P.

XX PR 08-AUG-2001; 2001US-0310801P.

XX PR 01-OCT-2001; 2001US-0326370P.

XX PR 04-DEC-2001; 2001US-0336780P.

XX PR 20-FEB-2002; 2002US-0358985P.


```
PA (ZYCO-) ZYCOS INC.
XX Chicx RM, Tomlinson AJ, Urban RG;
XX WPI; 2003-040607/03.
XX
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
XX cytoskeletal proteins, receptors or transcription factors), useful for
XX treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
XX leukemia.
XX
XX Example 2; SEQ ID NO 1861; 134pp; English.
XX
XX The invention describes a purified polypeptide, which comprises a
XX fragment of a kinase, phosphatase, protease, protease inhibitor,
XX transporter, cytoskeletal protein, receptor or transcription factor. The
XX polypeptide is useful as an immunogenic composition for eliciting in a
XX mammal an immunogenic response directed against any of the purified
XX polypeptide. The purified polypeptide, or the antibody that binds to this
XX polypeptide, is useful for treating cancer. The polypeptide is also
XX useful for identifying compounds that binds to a naturally processed
XX class I or class II MHC-binding polypeptide. The polypeptides and
XX polynucleotides are particularly useful for treating or preventing
XX myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
XX lymphoma or leukaemia. These are also useful for screening agents for
XX treating the above mentioned diseases. This sequence represents an
XX expressed protein tag (EPT) isolated from human tissue for translational
XX profiling. Note: This sequence does not appear in the printed
XX specification but was obtained in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 524 AA;
XX
XX Query Match 100.0%; Score 2789; DB 6; Length 524;
XX Best Local Similarity 100.0%; Pred. No. 4.6e-237;
XX Matches 524; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 MYAFLLASLLGAALAGPVLGKECTRGSAVWCQNVKTASDCGAVKHCLQTWNKPTVKS 60
Db 1 MYAFLLASLLGAALAGPVLGKECTRGSAVWCQNVKTASDCGAVKHCLQTWNKPTVKS 60
QY 61 LPCDICKDVTAAAGDMLKDNATEEILVYLEKTCDWLPKPNMSCKEIVDSILPVLDI 120
Db 61 LPCDICKDVTAAAGDMLKDNATEEILVYLEKTCDWLPKPNMSCKEIVDSILPVLDI 120
QY 121 IKGMSRPGEVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVVAPFMANIPLLY 180
Db 121 IKGMSRPGEVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVVAPFMANIPLLY 180
QY 181 PDGPRSKPQKNDGVDVCDCTQMTDITQAVRTNSTFVQALVEHVKEECDBLGFMDI 240
Db 181 PDGPRSKPQKNDGVDVCDCTQMTDITQAVRTNSTFVQALVEHVKEECDBLGFMDI 240
QY 241 CKNYISQYSEIAIQMMHMQPKEICALVGFCDVEKEMPQTLVPAKVASKNVIPALELVE 300
Db 241 CKNYISQYSEIAIQMMHMQPKEICALVGFCDVEKEMPQTLVPAKVASKNVIPALELVE 300
QY 301 PIKKHEVPKSDVYCEVCFVKEVTKLIDNNKTEKILDAFDKWCSPKLSLSECEQEV 360
Db 301 PIKKHEVPKSDVYCEVCFVKEVTKLIDNNKTEKILDAFDKWCSPKLSLSECEQEV 360
QY 361 VDTYGSISILLEEVSPELVCSMLHLCSTGLPALTVHVTQPKDGGFCEVCKLVGYLD 420
Db 361 VDTYGSISILLEEVSPELVCSMLHLCSTGLPALTVHVTQPKDGGFCEVCKLVGYLD 420
QY 421 RNLEKNSTQETLALEKCCSFLPDYQKQCFVAEYEPVLEIILVEWMDSPFVCLKITG 480
Db 421 RNLEKNSTQETLALEKCCSFLPDYQKQCFVAEYEPVLEIILVEWMDSPFVCLKITG 480
QY 481 ACPSAHKPLLTGTEKCIWGPSYWCNTETAAQCNVHECHKRWVN 524
Db 481 ACPSAHKPLLTGTEKCIWGPSYWCNTETAAQCNVHECHKRWVN 524
```

```
RESULT 13
ABU05199 standard; protein; 524 AA.
XX AC ABU05199;
XX
XX 29-JAN-2003 (first entry)
XX
XX Human expressed protein tag (EPT) #1865.
XX
XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
XX protease; protease inhibitor; transporter; cytoskeletal protein;
XX receptor; transcription factor; cancer; MHC;
XX major histocompatibility complex; myeloma; colon cancer; gastric cancer;
XX adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
XX Homo sapiens.
XX
XX WO200278524-A2.
XX
XX 10-OCT-2002.
XX
XX 28-MAR-2002; 2002WO-US009671.
XX
XX 28-MAR-2001; 2001US-0279495P.
XX
XX 21-MAY-2001; 2001US-0292544P.
XX
XX 08-AUG-2001; 2001US-0310801P.
XX
XX 01-OCT-2001; 2001US-0326370P.
XX
XX 04-DEC-2001; 2001US-0336780P.
XX
XX 20-FEB-2002; 2002US-0358985P.
XX
XX (ZYCO-) ZYCOS INC.
XX
XX Chicx RM, Tomlinson AJ, Urban RG;
XX
XX WPI; 2003-040607/03.
XX
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
XX cytoskeletal proteins, receptors or transcription factors), useful for
XX treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
XX leukemia.
XX
XX Example 2; SEQ ID NO 1865; 134pp; English.
XX
XX The invention describes a purified polypeptide, which comprises a
XX fragment of a kinase, phosphatase, protease, protease inhibitor,
XX transporter, cytoskeletal protein, receptor or transcription factor. The
XX polypeptide is useful as an immunogenic composition for eliciting in a
XX mammal an immunogenic response directed against any of the purified
XX polypeptide. The purified polypeptide, or the antibody that binds to this
XX polypeptide, is useful for treating cancer. The polypeptide is also
XX useful for identifying compounds that binds to a naturally processed
XX class I or class II MHC-binding polypeptide. The polypeptides and
XX polynucleotides are particularly useful for treating or preventing
XX myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
XX lymphoma or leukaemia. These are also useful for screening agents for
XX treating the above mentioned diseases. This sequence represents an
XX expressed protein tag (EPT) isolated from human tissue for translational
XX profiling. Note: This sequence does not appear in the printed
XX specification but was obtained in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 524 AA;
XX
XX Query Match 100.0%; Score 2789; DB 6; Length 524;
XX Best Local Similarity 100.0%; Pred. No. 4.6e-237;
XX Matches 524; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
```


QY 61 LPDCICKDVVTAAGDMLKDNATEEELVYLEKTCDWLPKPNMSASCKEIVDSYLPVILDI 120
DB |||||
QY 61 LPDCICKDVVTAAGDMLKDNATEEELVYLEKTCDWLPKPNMSASCKEIVDSYLPVILDI 120
DB |||||
QY 121 IKGEMSRPGEVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVAVPFMANIPALLEVE 180
DB |||||
QY 121 IKGEMSRPGEVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVAVPFMANIPALLEVE 180
DB |||||
QY 181 PDGPRSKPQPKDNGDVQCDCIQMVTDIQTAVRTNSTFVQALVEHVKECDRLGPGMADI 240
DB |||||
QY 181 PDGPRSKPQPKDNGDVQCDCIQMVTDIQTAVRTNSTFVQALVEHVKECDRLGPGMADI 240
DB |||||
QY 241 CKNYISOYSEIAIQMMHMQPKIEICALVGFCDVEKEMPQTLVPAKVASKNVIPALLEVE 300
DB |||||
QY 241 CKNYISOYSEIAIQMMHMQPKIEICALVGFCDVEKEMPQTLVPAKVASKNVIPALLEVE 300
DB |||||
QY 301 PIKKEHVPAKSDVYCEVCFVKEVTKLIDNNKTEKILDAFDKMCCKLPKLSSEECQEV 360
DB |||||
QY 301 PIKKEHVPAKSDVYCEVCFVKEVTKLIDNNKTEKILDAFDKMCCKLPKLSSEECQEV 360
DB |||||
QY 361 VDTYSSILSILLEEVSPELVCSMLHLCSTGTRLPALTAVHTVTPQKDGFCVCKLVGYLD 420
DB |||||
QY 361 VDTYSSILSILLEEVSPELVCSMLHLCSTGTRLPALTAVHTVTPQKDGFCVCKLVGYLD 420
DB |||||
QY 421 RNLEKNSTKQETILAALEKGCFLPDYPYQKQCFVAEYEPVLEIILVEVMDPSFVCLKIG 480
DB |||||
QY 421 RNLEKNSTKQETILAALEKGCFLPDYPYQKQCFVAEYEPVLEIILVEVMDPSFVCLKIG 480
DB |||||
QY 481 ACPSAHKPLLGTEKCIWGPSYWCQNTETAQAQCNVAHECKRHVWN 524
DB |||||
QY 481 ACPSAHKPLLGTEKCIWGPSYWCQNTETAQAQCNVAHECKRHVWN 524
DB |||||

RESULT 14
ABU05212
ID ABU05212 standard; protein; 524 AA.
XX AC ABU05212;
XX DT 29-JAN-2003 (first entry)
XX DE Human expressed protein tag (EPT) #1878.
XX KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX OS Homo sapiens.
XX PN WO200278524-A2.
XX PD 10-OCT-2002.
XX PF 28-MAR-2002; 2002WO-US009671.
XX PR 28-MAR-2001; 2001US-0279495P.
XX PR 21-MAY-2001; 2001US-0292544P.
XX PR 08-AUG-2001; 2001US-0310801P.
XX PR 01-OCT-2001; 2001US-0326370P.
XX PR 04-DEC-2001; 2001US-0336780P.
XX PR 20-FEB-2002; 2002US-0358985P.
XX PA (ZYCO-) ZYCOS INC.
XX PI Chiciz RM, Tomlinson AJ, Urban RG;
XX DR WPI; 2003-040607/03.
XX PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or

PT leukemia.
XX Example 2; SEQ ID NO 1878; 134pp; English.
XX The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for transla-
CC tional profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX Sequence 524 AA;

Query Match 100.0%; Score 2789; DB 6; Length 524;
Best Local Similarity 100.0%; Pred. No. 4.6e-237;
Matches 524; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MYALFLLASLLGAALAGPVILGKCTRGSVAVQNVKTRASDCGAVKHCLQTVNKPVTKS 60
DB |||||
QY 1 MYALFLLASLLGAALAGPVILGKCTRGSVAVQNVKTRASDCGAVKHCLQTVNKPVTKS 60
DB |||||
QY 61 LPDCICKDVVTAAGDMLKDNATEEELVYLEKTCDWLPKPNMSASCKEIVDSYLPVILDI 120
DB |||||
QY 61 LPDCICKDVVTAAGDMLKDNATEEELVYLEKTCDWLPKPNMSASCKEIVDSYLPVILDI 120
DB |||||
QY 121 IKGEMSRPGEVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVAVPFMANIPALLEVE 180
DB |||||
QY 121 IKGEMSRPGEVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVAVPFMANIPALLEVE 180
DB |||||
QY 181 PDGPRSKPQPKDNGDVQCDCIQMVTDIQTAVRTNSTFVQALVEHVKECDRLGPGMADI 240
DB |||||
QY 181 PDGPRSKPQPKDNGDVQCDCIQMVTDIQTAVRTNSTFVQALVEHVKECDRLGPGMADI 240
DB |||||
QY 241 CKNYISOYSEIAIQMMHMQPKIEICALVGFCDVEKEMPQTLVPAKVASKNVIPALLEVE 300
DB |||||
QY 241 CKNYISOYSEIAIQMMHMQPKIEICALVGFCDVEKEMPQTLVPAKVASKNVIPALLEVE 300
DB |||||
QY 301 PIKKEHVPAKSDVYCEVCFVKEVTKLIDNNKTEKILDAFDKMCCKLPKLSSEECQEV 360
DB |||||
QY 301 PIKKEHVPAKSDVYCEVCFVKEVTKLIDNNKTEKILDAFDKMCCKLPKLSSEECQEV 360
DB |||||
QY 361 VDTYSSILSILLEEVSPELVCSMLHLCSTGTRLPALTAVHTVTPQKDGFCVCKLVGYLD 420
DB |||||
QY 361 VDTYSSILSILLEEVSPELVCSMLHLCSTGTRLPALTAVHTVTPQKDGFCVCKLVGYLD 420
DB |||||
QY 421 RNLEKNSTKQETILAALEKGCFLPDYPYQKQCFVAEYEPVLEIILVEVMDPSFVCLKIG 480
DB |||||
QY 421 RNLEKNSTKQETILAALEKGCFLPDYPYQKQCFVAEYEPVLEIILVEVMDPSFVCLKIG 480
DB |||||
QY 481 ACPSAHKPLLGTEKCIWGPSYWCQNTETAQAQCNVAHECKRHVWN 524
DB |||||
QY 481 ACPSAHKPLLGTEKCIWGPSYWCQNTETAQAQCNVAHECKRHVWN 524
DB |||||

RESULT 15
ABU05213
ID ABU05213 standard; protein; 524 AA.
XX AC ABU05213;
XX DT 29-JAN-2003 (first entry)
XX

DE Human expressed protein tag (EPT) #1879.
XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX Homo sapiens.
XX WO200278524-A2.
XX 10-OCT-2002.
XX 28-MAR-2002; 2002WO-US009671.
XX 28-MAR-2001; 2001US-0279495P.
XX 21-MAY-2001; 2001US-0292544P.
XX 08-AUG-2001; 2001US-0310801P.
XX 01-OCT-2001; 2001US-0326370P.
XX 04-DEC-2001; 2001US-0336780P.
XX 20-FEB-2002; 2002US-0358985P.
XX (ZYCO-) ZYCO INC.
XX Chicx RM, Tomlinson AJ, Urban RG;
XX MPI, 2003-040607/03.
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX Example 2; SEQ ID NO 1879; 134pp; English.
XX The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX SQ

Query Match 100.0%; Score 2789; DB 6; Length 524;
Best Local Similarity 100.0%; Pred. No. 4.6e-237;
Matches 524; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MYALFLLASLLGAALAGPVLGKECTRGSAVNCQNVKTASDCGAVKHCLQTWNKPTVKS 60
Db 1 MYALFLLASLLGAALAGPVLGKECTRGSAVNCQNVKTASDCGAVKHCLQTWNKPTVKS 60
QY 61 LPCDICKDVTAAAGDMLKDNATEEILVYLEKTCDWLPKPNMSASCKEIVDSYLPVILDI 120
Db 61 LPCDICKDVTAAAGDMLKDNATEEILVYLEKTCDWLPKPNMSASCKEIVDSYLPVILDI 120
QY 121 IKGEMSRPGEVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVWAPFMANIPLLLY 180
Db 121 IKGEMSRPGEVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVWAPFMANIPLLLY 180
QY 181 PQDGRSKPQPKDNGDVQCDCIQWTTDIQTAVRTNSTFVQALVEHVKEECDRGLGPGMADI 240

Search completed: January 13, 2006, 16:30:19
Job time : 186.053 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 13, 2006, 16:23:49 ; Search time 41.6424 Seconds
(without alignments)
1210.728 Million cell updates/sec

Title: US-10-801-517-1
Perfect score: 2789
Sequence: 1 MVALFLASLLGALAGPVL.....NTETAAQCNAVEHCKRHVMN 524

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

PIR 80:.*
1: piri:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2777.5	99.6	527	1 SAHUP	saposin precursor
2	1996	71.6	554	1 A28716	saposin precursor
3	1937.5	69.5	557	1 JH0604	saposin precursor
4	511	18.3	965	2 T00207	P109 protein - sil
5	389	13.9	79	2 A49475	cerebroside sulfat
6	379	13.6	376	2 S02766	pulmonary surfacta
7	348.5	12.5	381	1 LNHUB	pulmonary surfacta
8	343	12.3	80	2 S21770	saposin-C - bovine
9	310	11.1	363	2 A29072	pulmonary surfacta
10	301.5	10.8	369	2 I46531	surfactant protein
11	261	9.4	81	2 A32026	glucosylceramide b
12	256.5	9.2	370	1 LNRBB	pulmonary surfacta
13	213	7.6	213	2 T46069	hypothetical prote
14	203.5	7.3	217	2 T48201	hypothetical prote
15	176.5	6.3	402	2 T15677	hypothetical prote
16	173.5	6.2	513	2 T09739	aspartic endopepti
17	171.5	6.1	506	2 F86253	hypothetical prote
18	165.5	5.9	506	2 T07915	probable aspartic
19	161.5	5.8	513	2 T11686	aspartic proteinas
20	161	5.8	428	2 S47096	cynarase (EC 3.4.2
21	161	5.8	474	2 T12049	cyprosin (EC 3.4.2
22	158.5	5.7	508	2 S19697	aspartic proteinas
23	156	5.6	314	2 T15674	hypothetical prote
24	155.5	5.6	292	2 T14446	aspartic proteinas
25	155.5	5.6	322	2 S41400	aspartic proteinas
26	154	5.5	496	2 S07332	aspartic proteinas
27	153.5	5.5	509	2 JC7272	aspartic proteinas
28	145.5	5.2	205	2 B89567	protein T08A9.7 [i
29	143.5	5.1	1175	2 S52417	E-selectin ligand-

ALIGNMENTS

RESULT 1

SAHUP

saposin precursor [validated] - human
N:Alternate names: cerebroside sulfate activator protein; co-beta-glucosidase; component ein (SAP); sphingolipid activator protein A2; sulfate sulfatase activator protein
N:Contains: prosaposin; saposin A; saposin B; saposin C; saposin D
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1992 #sequence revision 17-Nov-1995 #text change 09-Jul-2004
C:Accession: JX0061; A57368; A42003; B42003; D42003; A30367; S34740; S36140; S36
0226; I37265; I37264
R:Nakano, T.; Sandhoff, K.; Stuenkel, J.; Christomanou, H.; Suzuki, K.
J. Biochem. 105, 152-154, 1989
A:Title: Structure of full-length cDNA coding for sulfate activator, a Co-beta-glucosid
A:Reference number: JX0061; MUID:89255151; PMID:2498298
A:Accession: JX0061
A:Molecule type: mRNA
A:Residues: 1-527 <NA>
A:Cross-references: UNIPROT:P07602; UNIPARC:UPI000002B33D; GB:D00422; NID:g220063; PIDN
A:Note: alternative splice form 1
A:Accession: A57368
A:Molecule type: mRNA
A:Residues: 1-259,263-527 <NA2>
A:Cross-references: UNIPARC:UPI00000000DBF; GB:J03015; GB:J03086; NID:g337755; PIDN:AAB59
A:Note: alternative splice form 2
R:Rorman, E.G.; Scheinker, V.; Grabowski, G.A.
Genomics 13, 312-318, 1992
A:Title: Structure and evolution of the human prosaposin chromosomal gene.
A:Reference number: A42003; MUID:92307663; PMID:1612590
A:Accession: A42003
A:Molecule type: DNA
A:Residues: 50-140 <ROR>
A:Cross-references: UNIPARC:UPI00001741AA; GB:M86181
A:Note: sequence extracted from NCBI backbone (NCBIN:107235, NCBIP:107236)
A:Accession: B42003
A:Molecule type: DNA
A:Residues: 185-259;263-276 <RO2>
A:Cross-references: UNIPARC:UPI00001741AB; UNIPARC:UPI00001741AC
A:Note: sequence extracted from NCBI backbone (NCBIN:107235, NCBIP:107237)
A:Accession: C42003
A:Molecule type: DNA
A:Residues: 305-393 <RO3>
A:Cross-references: UNIPARC:UPI00001741AD
A:Note: sequence extracted from NCBI backbone (NCBIN:107235, NCBIP:107238); sequence inc
A:Accession: D42003
A:Molecule type: DNA
A:Residues: 399-487 <RO4>
A:Cross-references: UNIPARC:UPI00001741AE
A:Note: sequence extracted from NCBI backbone (NCBIN:107235, NCBIP:107239); sequence inc
R:Rorman, E.G.; Grabowski, G.A.
Genomics 5, 486-492, 1989
A:Title: Molecular cloning of a human co-beta-glucosidase cDNA: evidence that four spin
A:Reference number: A30367; MUID:90129043; PMID:2515150

cyprosin (EC 3.4.2
oryzasin (EC 3.4.2
gene 11-1 protein
probable aspartic
cag pathogenicity
hypothetical prote
aspartic proteinas
cysteine-rich fibr
hypothetical prote
cag island protein
aspartic proteinas
hypothetical prote
hypothetical prote
probable CHP-rich
hypothetical prote
rsec8 - rat (fragm

30 142.5 5.1 509 2 S49349
31 142.5 5.1 509 2 S6516
32 142.5 5.1 1948 2 S00485
33 141 5.1 508 2 D85056
34 134 4.8 1927 2 G64585
35 132.5 4.8 433 2 E96649
36 127.5 4.6 280 2 PC4080
37 127.5 4.6 1142 2 A45031
38 126.5 4.5 195 2 T15676
39 126.5 4.5 1819 2 A71928
40 126 4.5 506 2 S71591
41 123.5 4.4 370 2 E96502
42 119 4.3 661 2 S67177
43 116.5 4.2 652 2 F85017
44 116.5 4.2 707 2 T26218
45 116 4.2 975 2 I59422

Wed Jan 18 11:58:40 2006

A;Accession: A30367
A;Molecule type: mRNA
A;Residues: 1-259,263-527 <ROS>
A;Cross-references: UNIPARC:UPI00000000DBF; GB:J03077; NID:gl83230; PIDN:AAA52560.1; PID:9
A;Note: alternative splice form 2
R;Hiraiwa, M.; O'Brien, J.S.; Kishimoto, Y.; Galdzicka, M.; Fluharty, A.L.; Gimms, E.I.;
Arch. Biochem. Biophys. 304, 110-116, 1993
A;Title: Isolation, characterization, and proteolysis of human prosaposin, the precursor
A;Reference number: S34740; MUID:93311991; PMID:8323276
A;Accession: S34740
A;Molecule type: protein
A;Residues: 17-24;185-172;180-189;301-305 <HIR>
A;Cross-references: UNIPARC:UPI00001741B1; UNIPARC:UPI00001741B0; UNIPARC:UPI00001741B1;
R;Tynnelae, J.; Palmer, D.N.; Baumann, M.; Hallia, M.
PEBS Lett. 330, 8-12, 1993
A;Title: Storage of saposins A and D in infantile neuronal ceroid-lipofuscinosis.
A;Reference number: S36140; MUID:93380576; PMID:8370464
A;Accession: S36140
A;Molecule type: protein
A;Residues: 'XX', 62, 'X', 64-65, 'X', 67-79, 'X', 81-84 <TY>
A;Cross-references: UNIPARC:UPI00001741B3
A;Note: saposin A
A;Accession: S36141
A;Molecule type: protein
A;Residues: 'XXX', 413-414, 'X', 416-428, 'X', 430-434 <TY2>
A;Cross-references: UNIPARC:UPI00001741B4
A;Note: saposin D
R;Holtschmidt, H.; Sandhoff, K.; Kwon, H.Y.; Harzer, K.; Nakano, T.; Suzuki, K.
J. Biol. Chem. 266, 7556-7560, 1991
A;Title: Sulfatide activator protein. Alternative splicing that generates three mRNAs and
A;Reference number: S36988; MUID:91210267; PMID:2019586
A;Accession: S36988
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-240, 'S', 242-527 <HOL>
A;Cross-references: UNIPARC:UPI000016AFP6; EMBL:M60255; NID:g337759; PIDN:AAA36594.1; PI
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1991
A;Note: cerebroside sulfate activator protein mutant MU-9; corresponds to alternative sp
A;Accession: S36989
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-240, 'S', 242-259, 263-527 <HO2>
A;Cross-references: UNIPARC:UPI000016AFP7; EMBL:M60257; NID:g337764; PIDN:AAA36595.1; PI
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1991
A;Note: cerebroside sulfate activator protein mutant MU-0; corresponds to alternative sp
A;Accession: S36990
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-240, 'S', 242-259, 261-527 <HO3>
A;Cross-references: UNIPARC:UPI000016AFP8; EMBL:M60258; NID:g337766; PIDN:AAA36596.1; PI
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1991
A;Note: cerebroside sulfate activator protein mutant MU-6; corresponds to alternative sp
R;Kondoh, K.; Hienano, T.; Sano, A.; Kakimoto, Y.
Biochem. Biophys. Res. Commun. 181, 286-292, 1991
A;Title: Isolation and characterization of prosaposin from human milk.
A;Reference number: PS0330; MUID:92068206; PMID:1958198
A;Accession: PS0330
A;Molecule type: protein
A;Residues: 17-24, 'X', 26 <KON>
A;Cross-references: UNIPARC:UPI00001741B5
A;Experimental source: milk
R;Kretz, K.A.; Carlson, G.S.; Morimoto, S.; Kishimoto, Y.; Fluharty, A.L.; O'Brien, J.S.
Proc. Natl. Acad. Sci. U.S.A. 87, 2541-2544, 1990
A;Title: Characterization of a mutation in a family with saposin B deficiency: a glycosy
A;Reference number: A35985; MUID:90207231; PMID:2320574
A;Accession: A35985
A;Molecule type: mRNA
A;Residues: 213-221 <KRE>
A;Cross-references: UNIPARC:UPI00001741B6; GB:M32221
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-259,263-527 <KR2>

A;Cross-references: UNIPARC:UPI00000000DBF; GB:M32221; NID:g337761; PIDN:AAA60303.1; PID:9
A;Experimental source: lymphoblast
A;Accession: C35985
A;Molecule type: mRNA
A;Residues: 213-216, 'I', 218-221 <KR3>
A;Cross-references: UNIPARC:UPI00001741B7
A;Note: sequence from patients with activator-deficient metachromatic leukodystrophy; thi
R;Puerst, W.; Schubert, J.; Machleidt, W.; Meyer, H.E.; Sandhoff, K.
Eur. J. Biochem. 192, 709-714, 1990
A;Title: The complete amino-acid sequences of human ganglioside GM2 activator protein and
A;Reference number: S13195; MUID:91006165; PMID:2209618
A;Accession: S13196
A;Molecule type: protein
A;Residues: 195-259, 263-277 <FUE>
A;Cross-references: UNIPARC:UPI00001741B8
R;Morimoto, S.; Marcin, B.M.; Yamamoto, Y.; Kretz, K.A.; O'Brien, J.S.; Kishimoto, Y.
Proc. Natl. Acad. Sci. U.S.A. 86, 3389-3393, 1989
A;Title: Saposin A: second cerebroside activator protein.
A;Reference number: A32784; MUID:89240739; PMID:2717620
A;Accession: A32784
A;Molecule type: protein
A;Residues: 60-84;86-107;109-119;125-134 <MOR>
A;Cross-references: UNIPARC:UPI00001741B9; UNIPARC:UPI00001741BA; UNIPARC:UPI00001741BB;
R;O'Brien, J.S.; Kretz, K.A.; Dewji, N.; Wenger, D.A.; Esch, F.; Fluharty, A.L.
Science 241, 1098-1101, 1988
A;Title: Coding of two sphingolipid activator proteins (SAP-1 and SAP-2) by same genetic
A;Reference number: A41240; MUID:88321660; PMID:2842863
A;Accession: A41240
A;Molecule type: mRNA
A;Residues: 'GSSR', 18-259,263-299, 'D', 301-302, 'D', 304-527 <OAB>
A;Cross-references: UNIPARC:UPI00001741BD; GB:J03086
R;Dewji, N.N.; Wenger, D.A.; O'Brien, J.S.
Proc. Natl. Acad. Sci. U.S.A. 84, 8652-8656, 1987
A;Title: Nucleotide sequence of cloned cDNA for human sphingolipid activator protein 1 p
A;Reference number: S02289; MUID:88068647; PMID:2825202
A;Accession: S02289
A;Status: significant sequence differences
A;Molecule type: mRNA
A;Cross-references: EMBL:J03015
A;Note: this sequence corrected by A41240
A;Note: part of this sequence, including the amino end of the mature protein, was deter
R;Kleinschmidt, T.; Christomanou, H.; Braunitzer, G.
Biol. Chem. Hoppe-Seyler 369, 317-328, 1988
A;Title: Complete amino-acid sequence of the naturally occurring A(2) activator protein
A;Reference number: S02028; MUID:89207118; PMID:3242555
A;Accession: S02028
A;Molecule type: protein
A;Residues: 195-259,263-276 <KLE>
A;Cross-references: UNIPARC:UPI00001741BE
R;Fuerst, W.; Machleidt, W.; Sandhoff, K.
Biol. Chem. Hoppe-Seyler 369, 317-328, 1988
A;Title: The precursor of sulfatide activator protein is processed to three different p
A;Reference number: S00813; MUID:89000190; PMID:3048308
A;Accession: S00813
A;Molecule type: protein
A;Residues: 410-487 <FU2>
A;Cross-references: UNIPARC:UPI00001741BF
R;Kleinschmidt, T.; Christomanou, H.; Braunitzer, G.
Biol. Chem. Hoppe-Seyler 368, 1571-1578, 1987
A;Title: Complete amino-acid sequence and carbohydrate content of the naturally occurri
A;Reference number: S00226; MUID:88163077; PMID:3442600
A;Accession: S00226
A;Molecule type: protein
A;Residues: 314-393 <KL2>
A;Cross-references: UNIPARC:UPI000003EDBE
R;Vaccaro, A.M.; Salvioli, R.; Barca, A.; Tatti, M.; Ciaffoni, F.; Maras, B.; Siciliano
J. Biol. Chem. 270, 9953-9960, 1995
A;Title: Structural analysis of saposin C and B. Complete localization of disulfide bri
A;Reference number: A57297; MUID:95247790; PMID:7730378
A;Contents: annotation; disulfide bonds; glycosylation
R;Holtschmidt, H.; Sandhoff, K.; Fuerst, W.; Kwon, H.Y.; Schnabel, D.; Suzuki, K.
FEBS Lett. 280, 267-270, 1991
A;Title: The organization of the gene for the human cerebroside sulfate activator prote

A;Reference number: I37264; MUID:91192146; PMID:2013321

A;Accession: I37265

A;Status: translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 59-125 <RES>

A;Cross-references: UNIPARC:UPI000016A751; EMBL:X57107; NID:g30234; PIDN:CAA40391.1; PID

Query Match 99.6%; Score 2777.5; DB 1; Length 527;

Best Local Similarity 99.4%; Pred. No. 1.1e-175;

Matches 524; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 1 MYALFLASLLGALAGPVLGLKECTRGSAVWQNVKTASDCGAVKHCLQTVWVKPTVKS 60

DB 1 MYALFLASLLGALAGPVLGLKECTRGSAVWQNVKTASDCGAVKHCLQTVWVKPTVKS 60

QY 61 LPCDICKVVTAAAGDMLKDNATEBEILVLEKTCDWLPKPNMSACKSEIVDSYLPVILDI 120

DB 61 LPCDICKVVTAAAGDMLKDNATEBEILVLEKTCDWLPKPNMSACKSEIVDSYLPVILDI 120

QY 121 IKGEMSRPGEVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVVAPFMANIPLILY 180

DB 121 IKGEMSRPGEVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVVAPFMANIPLILY 180

QY 181 PDGPRSKPQKNGDVCDQCIQMTDITQAVRTNSTFVQALVEHVKECDRLGPGMADI 240

DB 181 PDGPRSKPQKNGDVCDQCIQMTDITQAVRTNSTFVQALVEHVKECDRLGPGMADI 240

QY 241 CKNYISQYSEIAIQMMHMQDPKBEICALVGFCDVEKEMPMQTLVPAKVASKNVIPALE 297

DB 241 CKNYISQYSEIAIQMMHMQDPKBEICALVGFCDVEKEMPMQTLVPAKVASKNVIPALE 300

QY 298 LVEPIKHEVPAKSDVYCEVFLVKEVTKLIDNNKTEKILDAFDKMCCKLPKSLSEEC 357

DB 301 LVEPIKHEVPAKSDVYCEVFLVKEVTKLIDNNKTEKILDAFDKMCCKLPKSLSEEC 360

QY 358 QEVDTYSSILSILLESVPELVCSMLHLCGSGTGLPALTVHVTPQKDGFCFVCKKLVG 417

DB 361 QEVDTYSSILSILLESVPELVCSMLHLCGSGTGLPALTVHVTPQKDGFCFVCKKLVG 420

QY 418 YLDRLNLEKNTKOEILAELEKCSLPDPYQKQCDQFVAEYEPVLIELVEMDPSFVCL 477

DB 421 YLDRLNLEKNTKOEILAELEKCSLPDPYQKQCDQFVAEYEPVLIELVEMDPSFVCL 480

QY 478 KIGACPSAHKPLGTKEKICWGPSYWCNTETAACQNAVEHCKRHWN 524

DB 481 KIGACPSAHKPLGTKEKICWGPSYWCNTETAACQNAVEHCKRHWN 527

RESULT 2

A28716

saposin precursor - rat

N;Alternate names: cerebroside sulfate activator protein; co-beta-glucosidase; component

ein (SAP); sphingolipid activator protein A2; sulfated glycoprotein 1; sulfatide sulfate

N;Contains: prosaposin; saposin A; saposin B; saposin C; saposin D

C;Species: Rattus norvegicus (Norway rat)

C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C;Accession: A28716

R;Collard, M.W.; Sylvestre, S.R.; Tsuruta, J.K.; Griswold, M.D.

Biochemistry 27, 4557-4564, 1988

A;Title: Biosynthesis and molecular cloning of sulfated glycoprotein 1 secreted by rat s

A;Reference number: A28716; MUID:89000647; PMID:3048385

A;Accession: A28716

A;Molecule type: mRNA

A;Residues: 1-554 <COL>

A;Cross-references: UNIPROT:P10960; UNIPARC:UPI000013555D; GB:M19936; NID:g206904; PIDN:

A;Note: parts of this sequence, including the amino end of the mature protein, were dete

C;Function:

A;Description: saposins bind sphingolipids, form hydrophilic complexes and make them acc

A;Pathway: sphingolipid catabolism

A;Note: saposin A (SAP-2) activate hydrolysis of glucocerebroside by beta-glucosy

A;Note: saposin B (SAP-1) activates hydrolysis of galactocerebroside sulfate by arylsulfi

A;Note: saposin D activates hydrolysis of sphingomyelin by sphingomyelin phosphodiester

C;Superfamily: saposin; saposin repeat homology

C;Keywords: alternative splicing; glycoprotein; lysosomal storage disease; lysosome; sph

F;1-16/Domain: signal sequence #status predicted <SIG>

F;17-554/Product: prosaposin #status predicted <PRO>

F;55-148/Domain: saposin repeat homology <SAP1>

F;60-143/Product: saposin A #status predicted <SAPA>

F;189-280/Domain: saposin repeat homology <SAP2>

F;194-273/Product: saposin B #status predicted <SAB1>

F;306-397/Domain: saposin repeat homology <SAP3>

F;310-389/Product: saposin C #status predicted <SAPC>

F;431-522/Domain: saposin repeat homology <SAP4>

F;437-514/Product: saposin D #status predicted <SAPD>

F;163-138,66-132,94-106,439-512,442-506,470-481/Diulfide bonds: #status predicted

F;180,214,331,456/Binding site: carbohydrate (Asn) (covalent) #status predicted

F;197-270,200-264,229-240,314-387,317-381,345-356/Diulfide bonds: #status predicted

Query Match 71.6%; Score 1996; DB 1; Length 554;

Best Local Similarity 66.3%; Pred. No. 4.2e-124;

Matches 368; Conservative 77; Mismatches 78; Indels 32; Gaps 3;

QY 1 MYALFLASLLGALAGPVLGLKECTRGSAVWQNVKTASDCGAVKHCLQTVWVKPTVKS 60

DB 1 MYALFLASLLGALAGPVLGLKECTRGSAVWQNVKTASDCGAVKHCLQTVWVKPTVKS 60

QY 61 LPCDICKVVTAAAGDMLKDNATEBEILVLEKTCDWLPKPNMSACKSEIVDSYLPVILDI 120

DB 61 LPCDICKVVTAAAGDMLKDNATEBEILVLEKTCDWLPKPNMSACKSEIVDSYLPVILDI 120

QY 121 IKGEMSRPGEVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVVAPFMANIPLILY 180

DB 121 IKGEMSRPGEVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVVAPFMANIPLILY 179

QY 181 PDGPRSKPQKNGDVCDQCIQMTDITQAVRTNSTFVQALVEHVKECDRLGPGMADI 240

DB 180 PDGPRSKPQKNGDVCDQCIQMTDITQAVRTNSTFVQALVEHVKECDRLGPGVSDI 239

QY 241 CKNYISQYSEIAIQMMHMQDPKBEICALVGFCDVEKEMPMQTLVPAKVASKNVIPALEIVE 300

DB 240 CKNYISQYSEIAIQMMHMQDPKBEICVWVGFCDVEKVPMTLVPAKVASKNVIPALEITD 299

QY 301 PIKHEVPAKSDVYCEVFLVKEVTKLIDNNKTEKILDAFDKMCCKLPKSLSEECQEV 360

DB 300 PYEQDVITQAOVNPFCVQVQVQLVMMKSELIINNATEILLIKGLSKACSLPAPATKQCEV 359

QY 361 VDTYSSILSILLESVPELVCSMLHLCGSG-----TRLP----- 394

DB 360 LVTFGPSLLDLVLEHVNPNFLCGVISLCSANPNLVGLEQPAIAIVSALPKPEAPPKQPE 419

QY 395 -----ALTVHVTPQKDGFCFVCKKLGYLDRLNLEKNTKOEILAELEKCSLPDPYQK 449

DB 420 EPKQSALRAHVPPQKNGFCFVCKKLGYLDRLNLEKNTKOEILAELEKCSLPDPYQK 479

QY 450 QCDQFVAEYEPVLIELVEMDPSFVCLKIGACPSAHKPLGTKEKICWGPSYWCNTETA 509

DB 480 QCDQFVAEYEPVLIELVEMDPSFVCLKIGACPSAHKPLGTKEKICWGPSYWCNTETA 539

QY 510 AQCNVAEHCKRHWN 524

DB 540 ARCNVAEHCKRHWN 554

RESULT 3

JH0604

saposin precursor - mouse

N;Alternate names: cerebroside sulfate activator protein; co-beta-glucosidase; component

ein (SAP); sphingolipid activator protein A2; sulfated glycoprotein 1; sulfatide sulfate

N;Contains: prosaposin; saposin A; saposin B; saposin C; saposin D

C;Species: Mus musculus (house mouse)

C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C;Accession: JH0604

R;Teuda, M.; Sakiyama, T.; Endo, H.; Kitagawa, T.

Biochem. Biophys. Res. Commun. 184, 1266-1272, 1992

A;Title: The primary structure of mouse saposin.

A;Reference number: JH0604; MUID:92272718; PMID:1590788

p109 protein - silkworm
C;Species: Bombyx mori (silkworm)
C;Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 09-Jul-2004
C;Accession: T00207
R;Tambunan, J.; Chang, P.K.; Li, H.; Natori, M.
Gene 212, 287-293, 1998
A;Title: Molecular cloning of a cDNA encoding a silkworm protein which contains the conserved
A;Reference numbers: 214124, MUID:98278844; PMID:9611271
A;Accession: T00207
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-965 <TAM>
A;Cross-references: UNIPROT:O15997; UNIPARC:UPI000007B54A; EMBL:AB008449; NID:92575864; I
P:778-870/Domain: saposin repeat homology <SAP3>

Query Match 18.3%; Score 511; DB 2; Length 965;
Best Local Similarity 24.6%; Pred. No. 7.5e-26;
Matches 139; Conservative 104; Mismatches 229; Indels 94; Gaps 18;

QY 19 VLGLKECTGSAVWCNVKTASDCGAVKHCLQTWNK---PTVKSLPCDICKVVTAAAGD 75
DB 170 LLGSRCTWGPSTWCSNFSSTGRECNATPHCINRVMSKMTFPEDNDNICQICLDMVKQAKD 229
QY 76 MLKDNATEBEILVYLEKTCMDLKPKNMSASCKEIVDSYLPVILDIKGMSPRGEVCSAL 135
DB 230 QLOSNETQDEIKVEFEGSKLPIKPFVARGCKMLADEFVVLEIETLASEWN-POAVCSVA 288
QY 136 NLCESS--LQKHIAELNHQKLES-----NKIPELDMTEVAVPFWA----- 173
DB 289 GLCNAKIDRLVLDYNAQRELKAGCYNCKTVGVVRKKPDETKYEDFLVGLLQVCRNMDS 348
QY 174 ---NIPLLYP-----QDG-----PRSKQPKDNGD 196
DB 349 LSDSCNMLIPKYVENILEAVKDLNPEGICHVSGQCSYKPHNHDEFTFPQMVQYSATDD 408
QY 197 V-QDCIQMTVDIQAVRTNSTFVQALVEHVKECDRLGPGMADICKNYISQYSEIAIQM 255
DB 409 VPCEPCQLVKHLRDLVLAANTTELE-FYKVLQGLCKQTGK-FKDECHLHAEQYYPVYNF 466
QY 256 MM-HMQPKGICALVGFCDVEKEMPMQTLV-----PAKVA-----SKNVIP 294
DB 467 LVSDLKPAETCKMTGICGNLTSAFISPLVARELVVQPKLIGABESKIARVPLAKQMEP 526
QY 295 ALELVE--PIKKHEVPA--KSDVYCEVCEFLVKEVTKLIDNNKTEKILDAFKMCKSLPK 351
DB 527 ASAAVSVLPLERMFVAAPQSKAACAFQCYFLHYLQVLSDTRTEDKVKAAVQAEACDALPD 586
QY 352 SLSEBCQEWVDYTGSSILSLLEBVSPELVCSMLHLCSTRLPALTVHTVQPKDGFCEV 411
DB 587 ALNGECKEFVTVQGSAAVIALVQEIHPASVCPALQICPQTE-EIRRVVNSEKSN--CPL 643
QY 412 CKKLGVYLDRLNKKSTQKIELAALKESCELPDPVQKQDQFVAEYEPVLJELVEVMD 471
DB 644 CLFAVEQLESVLKNNRSEBENIRKALDGLCTRLSLQKLSQCEIDFVDYSSQLVEMLVADWN 703
QY 472 PSFVCLKIGAC-PSAHKPLLGTEKCI 496
DB 704 AKEICVFLKLCRDQLDHPDLKLTHTSSI 729

RESULT 5
A49475
cerobroside sulfate activator - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 24-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 17-May-1996
C;Accession: A49475
R;Stevens, R.L.; Faull, K.F.; Conklin, K.A.; Green, B.N.; Fluharty, A.L.
Biochemistry 32, 4051-4059, 1993
A;Title: Porcine cerobroside sulfate activator: further structural characterization and
A;Reference number: A49475; MUID:93229506; PMID:8471613
A;Accession: A49475
A;Status: preliminary
A;Molecule type: protein

A;Accession: JH0604
A;Molecule type: mRNA
A;Residues: 1-557 <TSU>
A;Cross-references: UNIPROT:O61207; UNIPARC:UPI0000170C25; GB:S36200; NID:9249386; PIDN:
A;Experimental source: liver
C;Function:
A;Description: saposins bind sphingolipids, form hydrophilic complexes and make them acc
A;Pathway: sphingolipid catabolism
A;Note: saposins A and C (SAP-2) activate hydrolysis of glucocerebroside by beta-glucosyl
A;Note: saposin B (SAP-1) activates hydrolysis of galactocerebroside sulfate by arylsulfa
A;Note: saposin D activates hydrolysis of sphingomyelin by sphingomyelin phosphodiester
A;Superfamily: saposin; saposin repeat homology
C;Keywords: alternative splicing; glycoprotein; lysosomal storage disease; lysosome; sph
C;Keywords: signal sequence #status predicted <SIG>
F:1-16/Domain: saposin repeat homology <SAP1>
F:17-557/Product: prosaposin #status predicted <PRO>
F:50-143/Domain: saposin A #status predicted <SAPA>
F:55-148/Domain: saposin B #status predicted <SAB1>
F:60-143/Product: saposin B #status predicted <SAB1>
F:189-283/Domain: saposin C #status predicted <SAP3>
F:194-276/Product: saposin C #status predicted <SAP3>
F:309-400/Domain: saposin C #status predicted <SAPC>
F:313-392/Product: saposin C #status predicted <SAPC>
F:434-525/Domain: saposin repeat homology <SAP4>
F:434-525/Product: saposin D #status predicted <SAPD>
F:440-517/Product: saposin D #status predicted <SAPD>
F:63-138,66-132,94-106,197-273,200-267,229-240,317-390,320-384,348-359,442-515,445-509,4
F:80,214,334,379,459/Binding site: carbohydrate (Aen) (covalent) #status predicted

Query Match 69.5%; Score 1937.5; DB 1; Length 557;
Best Local Similarity 63.6%; Pred. No. 3.1e-120;
Matches 355; Conservative 77; Mismatches 91; Indels 35; Gaps 3;

QY 1 MYALFLASLGAALAGVLGLKECTGSAVWCNVKTASDCGAVKHCLQTWNKPTVKS 60
DB 1 MYALFASLLATALTSPVQPKTCGSGSALVLCRDVKTAVDCGAVKHCCQMVWSEKPTAKS 60
QY 61 LPDICTKDVVTAAGDMLKDNATEBEILVYLEKTCMDLKPKNMSASCKEIVDSYLPVILDI 120
DB 61 LPDICTKVTVEAGNLLKDNATQBEILHYLEKTCSEIHDSSLSASCKEIVDSYLPVILDM 120
QY 121 IKGNSRGEVCSALNLCELSQKHIAELNHQKLESNKIPELDMTEVAVPFWANIPLLLY 180
DB 121 IKGNSNPFGEVCSALNLCSLQSLQVLAQN-QKLESNKIPEVDMARVAVPMSNIPLLLY 179
QY 181 PDGPRSKPQKONGDVQDCDCTQMTVDIQAVRTNSTFVQALVEHVKECDRLGPGMADI 240
DB 180 PDHPRSQOPQRANEDVCQCMKLVSDVQTAVKTNSSFTQGFVDHVKECDRLGPGVSDI 239
QY 241 CKNYISQYSEIAIQMNMH---QPKIEICALVGFCDVEKEMPMQTLVPAKVASKNVIPAILE 297
DB 240 CKNYVDYSEVVCQMLNMHQDQPKIEICVLGFCNEVRVPMKTLVPATETIKNIPALILE 299
QY 298 LVPEPKKHEVPAKSDVYCEVCEFLVKEVTKLIDNNKTEKILDAFKMCKSLPKSLSEBC 357
DB 300 MMDPEYNLVQAHVILLCQTCQFVWAKFSELIYNNATEELLVKGLSNACGLVPDPARTKC 359
QY 358 QEVVDYTGSSILSLLEBVSPELVCSMLHLCSTG----- 390
DB 360 QEVVGTGFPBLLDIFIHEVNPSSLCGVIGLCAARPELVLEQAPPAIVSALLKEPTPPK 419
QY 391 ----TRLPALTVHTVQPKDGFCEVCKKLGVYLDRLNKKSTQKIELAALKESCELPDP 446
DB 420 QPAQPKQSALPAHVPPQKNGGFCVCKKLVLVLEHNLKKNSTKEEILAALEKSGCSFLPDP 479
QY 447 YQKQCDQFVAEYEPVLJELVEVMDPSFVCLKIGACPSAHKPLLGTEKCTWGPSTWQNT 506
DB 480 YQKQCDQFVAEYEPVLJELVEVMDPFGVCSKIGVCSAYKLLLGTEKCVWGSPYWCNM 539
QY 507 ETAAQCNVAVHCKRHVN 524
DB 540 ETAAQCNVAVHCKRHVN 557

RESULT 4
T0207

A;Residues: 1-79 <STE>
A;Cross-references: UNIPARC:UPI0000177938
A;Experimental source: kidney
A;Note: sequence extracted from NCBI backbone (NCBIP.129597)
C;Superfamily: saposin; saposin repeat homology
F;1-79/Domain: saposin repeat homology <SAP>

Query Match 13.9%; Score 389; DB 2; Length 79;
Best Local Similarity 88.6%; Pred. No. 3.6e-19;
Matches 70; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 195 GDVQDCIQWTDIQAVRTNSTFVQALVHVHKECDRLGPGNADICKNYISQYSIAIQ 254
DB 1 GDVQDCIQWTDIQAVRTNSTFVQALVHVHKECDRLGPGNADICKNYISQYSIAIQ 60

QY 255 MMHMQPKICALVGCDE 273
DB 61 MMHMQPKICGLVGCDE 79

RESULT 6
S02766
pulmonary surfactant protein B precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 09-Jul-2004
C;Accession: S02766
R;Enrie, P.A.; Shannon, J.M.; Mason, R.J.; Fisher, J.H.
Biochim. Biophys. Acta 994, 215-221, 1989
A;Title: cDNA and deduced amino acid sequence for the rat hydrophobic pulmonary surfactant protein B
A;Reference number: S02766; MUID:89150284; PMID:2920185
A;Accession: S02766
A;Molecule type: mRNA
A;Residues: 1-376 <EMR>
A;Cross-references: UNIPROT:P22355; UNIPARC:UPI00001327P8; EMBL:X14778; NID:g57284; PIDN:191-269/Domain: saposin repeat homology
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-190/Domain: propeptide #status predicted <PRO>
F;59-151/Domain: saposin repeat homology <SAP1>
F;190-277/Domain: saposin repeat homology <SAP2>
F;191-269/Domain: saposin repeat homology <SAP3>
F;286-371/Domain: saposin repeat homology <SAP3>

Query Match 13.6%; Score 379; DB 2; Length 376;
Best Local Similarity 22.6%; Pred. No. 1.2e-17;
Matches 116; Conservative 75; Mismatches 158; Indels 164; Gaps 16;

QY 4 LFLASILGAAAGPVLGKECTRGSAVWQNVKTASDCGAVKHCLQTVNKPVKSLPC 63
DB 9 LLLPFLCSLGAATESASSPDCAQGPKEWCSLEQAIQCFALGHLQEVWGHAGANDL-C 67

QY 64 DIQDVVTAAGDMLKONATEBEILVLEKTCWMLPKPNMSASCKEIVDSYLPVILDIK 123
DB 68 QECEDIVHLLTKMTKEDAFQDTIRKFLQECQDILPLKLVPRCQVLDVYLPVIFYFQ 127

QY 124 EMSPRGVCSALNLCESLQHLAELNHQKLESNKIPELMDTEVWAPPFMANIPILLVPOD 183
DB 128 QI-KPKAICSHVGLC-----PE-----GQT 146

QY 184 GPRSKFQPKDNGDVQDCQIQWTDIQAVRTNSTFVQALVHVHKECDRLGPGNADICKN 243
DB 147 KPEQKPE----- 153

QY 244 YISQYSIAIQMMHMQPKICALVGCDEKMPQTLVPAKVASKNVTPALE-----LVE 300
DB 154 -----MLDAIENPLLNKLVLPALPGAPLAR 178

QY 301 P-----IKKHEVPAKSDVYCEVCEFLVKEVTKLIDNNKTEKTLID-AFDKMCCKLPKSL 353
DB 179 PGPHTDLSBQQLPDIP-LP-FWLCRTLLIKKQAVI-----PKGVLAIVASQVCHVPLVV 232

QY 354 SEECQEVVDYVGSILSILLESPELVCSMLHLC-----GTRLPALTVHVTVQ-PKDG 407
DB 233 GGICQCLAEYTVLLDALLGRVVPQVLCGLVLECSADAIGPALPALEPIEKWPLQDT 292

QY 408 FCEVCKKLVGYLDRNLKNSTKQETLAALKEKC-SFLPPYQKQCDQFVAEYEPVLIEL 466
DB 293 ECHFCKSVI-----NQAWNTSQAMPOAMHQACLRFLWD--RQKCEQFVEQHMPOLLALV 345

QY 467 VEVMPSPFVCLKIGACPSAHKPLLTGTEKICWGP 499
DB 346 PRSQAHTSCQALGVCEAPASPL-----QCFQTP 374

RESULT 7
LNHUB
pulmonary surfactant protein B precursor [validated] - human
N;Alternate names: pulmonary surfactant proteolipid SP-B; pulmonary surfactant-associate
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Jul-2004
C;Accession: A31361; A28461; A27794; A27592; JU0162; S21134
R;Pilot-Matias, T.J.; Kister, S.E.; Fox, J.L.; Kropp, K.; Glasser, S.W.; Whitsett, J.A.
DNA 8, 75-86, 1989
A;Title: Structure and organization of the gene encoding human pulmonary surfactant protein B
A;Reference number: A31361; MUID:89170128; PMID:2924687
A;Accession: A31361
A;Molecule type: DNA
A;Residues: 1-381 <PIL>
A;Cross-references: UNIPROT:P07988; UNIPARC:UPI00001423D4; GB:M24461
A;Note: the codon given for residue 131 (ATT) is inconsistent with the authors' translation
R;Jacobs, K.A.; Phelps, D.S.; Steinbrink, R.; Fisch, J.; Kriz, R.; Mitsock, L.; Dougher, J.
J. Biol. Chem. 262, 9808-9811, 1987
A;Title: Isolation of a cDNA clone encoding a high molecular weight precursor to a 6-kDa
A;Reference number: A28461; MUID:87250653; PMID:3597440
A;Accession: A28461
A;Molecule type: mRNA
A;Residues: 1-227, 'A', 229-381 <JAC>
A;Cross-references: UNIPARC:UPI00000162D; GB:J02761; NID:g190673; PIDN:AAA60212.1; PID
A;Note: part of this sequence, including the amino end of the mature protein, was confi
R;Glasser, S.W.; Korfhagen, T.R.; Weaver, T.; Pilot-Matias, T.; Fox, J.L.; Whitsett, J.
Proc. Natl. Acad. Sci. U.S.A. 84, 4007-4011, 1987
A;Title: cDNA and deduced amino acid sequence of human pulmonary surfactant-associate
A;Reference number: A27794; MUID:87231940; PMID:3035561
A;Accession: A27794
A;Molecule type: mRNA
A;Residues: 'EPR', 99-317, 'L', 319-381 <GLA>
A;Cross-references: UNIPARC:UPI000014237D; GB:M16764; NID:g338410; PIDN:AAA88099.1; PID
A;Note: 131-ile was also found
A;Note: part of this sequence, including the amino end of the mature protein, was confi
R;Revak, S.D.; Merritt, T.A.; Degryse, E.; Stefani, L.; Courtney, M.; Hallman, M.; Coch
J. Clin. Invest. 81, 826-833, 1988
A;Title: Use of human surfactant low molecular weight apoproteins in the reconstitution
A;Reference number: A27592; MUID:88139786; PMID:3343343
A;Accession: A27592
A;Molecule type: mRNA
A;Residues: 139-177, 'V', 179-227, 'A', 228-381 <REV>
A;Cross-references: UNIPARC:UPI00001741A7; GB:M19097
A;Note: part of this sequence, including the amino end of the mature protein, was confi
A;Note: the mature protein (SP 18) consists of two identical disulfide-bonded 9K polype
R;Nizumoto, M.; Adachi, H.
Sapporo Igaku Zaasshi 56, 731-742, 1987
A;Title: Primary structure of a hydrophobic 6kDa apoprotein (SP6) of human pulmonary su
A;Reference number: JU0162
A;Accession: JU0162
A;Molecule type: protein
A;Residues: 201-207, 'X', 209-210, 'X', 212-227, 'A', 229-234, 'X', 236-245, 'X', 247, 'L', 249-253
A;Cross-references: UNIPARC:UPI00001741A8
R;Johansson, J.; Joernvall, H.; Curstedt, T.
FEBS Lett. 301, 165-167, 1992
A;Title: Human surfactant polypeptide SP-B. Disulfide bridges, C-terminal end, and pept
A;Reference number: S21134; MUID:92233937; PMID:1568474
A;Accession: S21134
A;Status: preliminary
A;Molecule type: protein
A;Residues: 201-227, 'I', 229-279 <JOH>
A;Cross-references: UNIPARC:UPI00001741A9

A>Note: 228-Ala was also found
C:Comment: Pulmonary surfactant is a complex of phospholipids and proteins that lowers t
C:Genetics:
A:Gene: GDB:SFTPB; SFTP3; SP-B
A:Cross-references: GDB:I20374; OMTM:178640
A:Map position: 2p12-2p11.2
A:Introns: 23/1; 65/3; 89/3; 131/3; 194/3; 224/3; 286/1; 334/3; 361/3
C:Superfamily: pulmonary surfactant protein B; saposin repeat homology
C:Keywords: alveolar proteinosis; gaseous exchange; glycoprotein; lipoprotein; lung; pul
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-200/Domain: propeptide #status predicted <PRO>
F:61-153/Domain: saposin repeat homology <SAP1>
F:200-287/Domain: saposin repeat homology <SAP2>
F:201-279/Product: pulmonary surfactant protein B, 9K form #status predicted <SP9>
F:201-256/Product: pulmonary surfactant protein B, 6K form #status experimental <SP6>
F:291-376/Domain: saposin repeat homology <SAP3>
F:69-143,72-137,100-112,299-366,302-360,325-335/Disulfide bonds: #status predicted
F:129,311/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:208-277,211-271,235-246/Disulfide bonds: #status experimental
F:248/Disulfide bonds: interchain #status experimental

Query Match 12.5%; Score 348.5; DB 1; Length 381;
Best Local Similarity 21.6%; Pred. No. 1.2e-15;
Matches 111; Conservative 72; Mismatches 171; Indels 161; Gaps 16;

Qy 2 VALFLLASLILGAALAGPVILGLKECTRGSAVWQNVKTASDCGAVKHCLQTVNNKPTVKS 61
Db 9 WLLLLPTLCGPTAAWTSSLACAGPEFWQSLEALQCRALGHCLQEVWGHVGADDL 68

Qy 62 PCDICDVVTAAGMDKDNATEBEILVYLEKTCWMLPKPNMSASCKEIVDSYLPVILDI 121
Db 69 -COECEDIVHILNKWAKEAIFQDTRKFLQECNVLPKLMPQCQNVLDYFPLVIDYF 127

Qy 122 KEEMSRPGEVCSALNCLCSLQKHLAEINHQLESNKIPELDMTEVVAFFMANIPLLLYP 181
Db 128 QNQTDSNG-ICMHLGLCKSRQ----- 147

Qy 182 QDGRSKPQPKDNGDVQCDCIQWTDIQTAVRTNSTFVQALVEHVKEECDRLGPGWADIC 241
Db 148 -----PEPEQE-----PGMSD-- 158

Qy 242 KNYISQYSBIAIOMMHMOPKEICALVGFCDVEKMPQTLVPAKVASKNVTPALELVEP 301
Db 159 -----PLPK-----PLRDLPLDPLDLKLVLELP--GA 184

Qy 302 IKKHEVPAKSDV-----YCEVCEFLVKEVTYKLDNNKTEKILDAFDKMSCKLPK 351
Db 185 LQARPGPHQTDLSEQQFPPLPYCMLCRALIKRIQMIPIKG-----ALRVAVAQVCRVPL 240

Qy 352 SLSECEQVVDVTYVSSILSILLESVPVCSMLHCLS-----GTRLPALTVHVTPQKDG 406
Db 241 VAGGICQCLAEYSVILLDTLGRMLPQLVCLRVLECSWDSAGPRSP---TGEMLPKDS 297

Qy 407 GFCEVCKLGVLDRLNLEKNSTKQETLAALKEGC--SFILPDYQKQCDQFVAYEYFVLIE 464
Db 298 E-CHLCMSVT-----TQAGNSBEOAIPQAMQACVGSWLD---RBKCKQFVEQHTPQLIT 348

Qy 465 ILVEMDPSFVCLKIGACPSAHKPLLGTEKCIWGP 499
Db 349 LVPRGWDHATTTCQALGVCGTMSPL-----QCIHSP 379

RESULT 8
S21770
saposin-C - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 31-Oct-1997
C:Accession: S21770
R:Sano, A.; Mizuno, T.; Kondoh, K.; Hineno, T.; Ueno, S.; Kakimoto, Y.; Morita, N.
Biochim. Biophys. Acta 1120, 75-80, 1992
A:Title: Saposin-C from bovine spleen; complete amino acid sequence and relation between
A:Reference number: S21770; MUID:92207994; PMID:1554743
A:Accession: S21770

A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-80 <SAN>
A:Cross-references: UNIPARC:UPI0000177939
C:Superfamily: saposin; saposin repeat homology

Query Match 12.3%; Score 343; DB 2; Length 80;
Best Local Similarity 79.7%; Pred. No. 3.9e-16;
Matches 63; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

Qy 311 SDVYCEVCEFLVKEVTYKLDNNKTEKILDAFDKMSCKLPKSLSECEQVVDVTYVSSILS 370
Db 1 ADYQVCEFWKEVAVKLDNNRTEBEILHALDKVCSKLPSTSLAEQCEQVVDVTYVGRSILS 60

Qy 371 ILLEEVSPVCSMLHCLS 389
Db 61 ILLDEASPELVCSMLHCLS 79

RESULT 9
A29072
pulmonary surfactant protein SP 18 precursor - dog (fragment)
C:Species: Canis lupus familiaris (dog)
C:Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 09-Jul-2004
C:Accession: B29072; A29072
R:Hawgood, S.; Benson, B.J.; Schilling, J.; Damm, D.; Clemente, J.A.; White, R.T.
Proc. Natl. Acad. Sci. U.S.A. 84, 66-70, 1987
A:Title: Nucleotide and amino acid sequences of pulmonary surfactant protein SP 18 and e
A:Reference number: A29072; MUID:87092398; PMID:3467361
A:Accession: B29072
A:Molecule type: mRNA
A:Residues: 1-363 <HAW>
A:Cross-references: UNIPROT:P17129; UNIPARC:UPI00001327F3; GB:M15170; NID:G164077; PIDN:
A:Accession: A29072
A:Molecule type: protein
A:Residues: 182-210 <HAW>
A:Cross-references: UNIPARC:UPI0000177937
C:Superfamily: pulmonary surfactant protein B; saposin repeat homology
F:1-14/Domain: signal sequence #status predicted <SIG>
F:15-180/Domain: propeptide #status predicted <PRP>
F:54-146/Domain: saposin repeat homology <SAP1>
F:180-267/Domain: saposin repeat homology <SAP2>
F:181-363/Product: pulmonary surfactant protein SP 18 #status experimental <MAT>
F:273-358/Domain: saposin repeat homology <SAP3>

Query Match 11.1%; Score 310; DB 2; Length 363;
Best Local Similarity 22.0%; Pred. No. 3.9e-13;
Matches 112; Conservative 76; Mismatches 161; Indels 160; Gaps 20;

Qy 4 LFLASL--LGAA--LAGPVILGLKECTRGSAVWQNVKTASDCGAVKHCLQTVNNKPTVKS 60
Db 4 LLLPLTLCGLGAADWSAFSLA---CARGPAFWCOSLEALQCRALGHCLQEVWGNARADD 60

Qy 61 LPCDICDVVTAAGMDKDNATEBEILVYLEKTCWMLPKPNMSASCKEIVDSYLPVILDI 120
Db 61 L-CQECQDIVILITKWTKEAIFQDWRVFLHEHCDVLPKLTTPQCHEMLGTYFFVVDY 119

Qy 121 IKGEMSRPGEVCSALNCLCSLQKHLAEINHQLESNKIPELDMTEVVAFFMANIPLLLY 180
Db 120 FQSQIN-PKIIICKHLGLC---KPGPEPEQSELSPLDLKLLPEL----- 162

Qy 181 PDGPRSKPQPKDNGDVQCDCIQWTDIQTAVRTNSTFVQALVEHVKEECDRLGPGMADI 240
Db 163 -----PGALQV 168

Qy 241 KKNYISQYSBIAIOMMHMOPKEICALVGFCDVEKMPQTLVPAKVASKNVTPALELVE 300
Db 169 TGFPTQDUSE-----QQLP-----IP----- 184

Qy 301 PIKKEHVPAKSDVYCEVCEFLVKEVTYKLDNNKTEKILD-AFDKMSCKLPKSLSECEQ 359
Db 185 -----LP-----YCWLCRTLLIKRIQAMI-----PKGVLAVTVGVCHVPLVVGICQC 228

Db 131 QINAKA-ICQHLGLCQ-----FCSPEPPPLD-----PLPDKLVLPITLL---G 167

Qy 184 GPRSKPQKNDGVCQDCIQMTDITQAVRTNSTFQVALVEHVKEBCDRDLGFGMADICKN 243

Db 168 ALPAKGP----- 175

Qy 244 YISQSEIAIQMMHQPKKEICALVGFCDEVKEMPMQTLVPAKSKNVIPALELVEPIK 303

Db 176 -----HTQ-----DLSAQPPPIPLP----- 190

Qy 304 KHEVPAKSDVYCEVCEFLVKEVTKLIDNNKTEKILD-AFDKMSKLPKLSSECEQVVD 362

Db 191 -----LCWLCTLLAKRIQMI-----PKGVLANAVAQVCHVPLVVGICQCLAE 235

Qy 363 TYGSIILSILLESVPELVCSMLHLS-----GTRLPALTVHVTQ---PKDGGFCEVCKKL 415

Db 236 RYTVILLEVLLGHVLPQLVGLVLRCSVDISQVPTLEALPGEWLPQDPE-CRLQMSV 294

Qy 416 VGYLDRLNLEKNSKQEIILAA-----LEKGSFLPDYKQKQCDQFVAEYEPVLIIELVEM 470

Db 295 TTQA-RNISEQTRQAVYHACLSSQLD-----QECEQFVAHAP-----AA 335

Qy 471 DPFVCLKIGACPSAHKPELLGTE-----KCIINGPSY 501

Db 336 EFAVQGL---GCP---RNLPGEGRVATLSPLOCIQSPHF 370

RESULT 13

T46069

hypothetical protein T18N14.110 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004

C:Accession: T46069

R:Deleeny, M.; Berger, C.; Cooke, R.; Grellet, F.; Laudie, M.; Mewes, H.W.; Lemcke, K.;

submitted to the Protein Sequence Database, December 1999

A:Reference number: Z23013

A:Accession: T46069

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-213

A:Cross-references: UNIPROT:Q9SCTS; UNIPARC:UPI00000AC273; EMBL:AL132968

A:Experimental source: cultivar Columbia, BAC clone T18N14

C:Genetics:

A:Map position: 3

A:Introns: 31/1; 80/3; 146/3; 166/3

A>Note: T18N14.110

Query Match 7.6%; Score 213; DB 2; Length 213;

Best Local Similarity 25.7%; Pred. No. 5e-07; Indels 10; Gaps 6;

Matches 57; Conservative 35; Mismatches 90;

Qy 292 VIPALELVEPIKHEVPAKSDVYCEVCEFLVKEVTKLIDNNKTEKILDADKMSKLPK 351

Db 18 VSDARSFVDSITSEKVNKEDV-CTLCEEYVTDALSYLEKNVTQAEIIEDLHDCSQL-R 75

Qy 352 SLSECEQVWDTYGSISILLESVPELVCSMLHLSGTPLPALTVHVTQPKDGGFCEV 411

Db 76 GYSQCISLVDDY-VPLFPLQLESQPHYFCRMNLGC--KVVALVEEARQDS-----CGV 128

Qy 412 CKKLVGYLDRLNLEKNSKQEIILAALEKGSFLPDYKQKQCDQFVAEYEPVLIIELVEMD 471

Db 129 CHRTVSEIILKLODPDQLDIVELLIKGCKSLKN-YEKKCKTLVFEYGYGLVNVNAEPLV 187

Qy 472 PSFVCLKIGACP 483

Db 188 KNDVCTLLRACP 199

RESULT 14

T48201

hypothetical protein T20L15.70 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Text change 09-Jul-2004

C;Accession: T48201
R;Bavan, M.; Peters, S.A.; van Staveren, M.; Dirkse, W.; Stiekema, W.; Bancroft, I.; Mew,
submitted to the Protein Sequence Database, March 2000

A;Reference number: Z24488

A;Accession: T48201

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-217 <BEV>

A;Cross-references: UNIPROT:Q9LZW6; UNIPARC:UIP00000A6022; EMBL:AL162351

A;Experimental source: cultivar Columbia; BAC clone T20L15

C;Genetics:

A;Map position: 5

A;Introns: 30/1; 79/3; 146/3; 166/3

A;Note: T20L15.70

Query Match
Best Local Similarity 7.3%; Score 203.5; DB 2; Length 217;
Matches 52; Conservative 40; Mismatches 82; Indels 13; Gaps 7;

QY 298 LVEPTKK-HEVPKASDVCEVFPELVKEVTKLIDNNNTEKEILDAFDKMCKSLPKSLSSE 356
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 298 LLEPPESAH-----DNQCVELCDKVTVLDIQLDYDQNELVEALHISCSQIP-PLKKQ 79

QY 357 QGVVDYTGSSTILLSLLREVSPSELVCMHLSCGTGLPALTVTHTQPDKGPGCEVCCKLY 416
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 357 CUSMDWHY-TQLFPTQSIVTSIKSDOICKRLNLCAV--TPAFASQVHQ---GNCEACKRET V 133

QY 417 GVLDNRLENKSNTOETILAIEKCPSFLDPYPQQKQCFVAEYPEPVLTITIELVMNDPSFVC 476
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 417 SEVVTKLPDEPETKIIRLLLKEKSL-NNYQDKCKWFEYGFLMLTDLQKFLEKXDCV 192

QY 477 LKIGACP 483
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 477 TLHFVCP 199

RESULT 15

Tl5677

Hypothetical protein C28C12.5 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004

C;Accession: Tl5677

R;Miller, N.

E;Submitted to the EMBL Data Library, November 1995

A;Description: The sequence of C. elegans cosmid C28C12.

A;Reference number: Zl8387

A;Accession: Tl5677

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-402 <MI>

A;Cross-references: UNIPROT:Q18279; UNIPARC:UIP0000076C88; EMBL:U40797; NID:g1065916; P

A;Experimental source: strain Bristol N2; clone C28C12

C;Genetics:

A;Gene: CESP:C28C12.5

A;Map position: 4

A;Introns: 29/3; 82/3; 124/3; 151/3; 258/3; 318/1; 372/3; 400/3

Query Match
Best Local Similarity 6.3%; Score 176.5; DB 2; Length 402;
Matches 75; Conservative 58; Mismatches 156; Indels 81; Gaps 15;

QY 184 GPBSKPQRKDNGDVQCDCIQMTVIDQTAVRTNSTFTVALYEHVKEECDRLGGMGADICKN 243
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 184 GAQAASP-----CESCKSMVNQTFDASKDRMKMAQLKVS-LSMLC-VGTSHSQDSCK 66

QY 244 YISQYSFIATQMAMHM-QPKIEICALVGFCDEVKEMPQTLPAPAKVSKNVIPALELVEPI 302
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 244 TLCLKLFIAVLAPYLADTSAVCSKLGMCGESQSFSLARLANLYLKSEAIVA---NDNI 123

QY 303 KGHVPAKSVDYCEVCEFLVKEVTKLIDNNNTEKEILDAFDKMCKSLPKSLSSECQEVD 362
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 303 MRGEV-----CDECQAATAQIGKLVGDFTTYAVKSTLRQRFVFKSAGAKAAC----N 172

```
QY 363 TYGSSILSILLEEV-----SPELVCSMLHLCSGTRLPALTVHVTPKDGCGFCEVCKKLVG 417
Db : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
173 IFVSSVIPDLMTMKDMFTKELMCSNMGLCSATSKPAAREAPKQPAS-----EMWKSMM-- 226
QY 418 YLDRNLEKNSTKQEIILAALEKGCFLDPYQKQ----- 450
Db : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
227 ----GMVXTSNGEELMSCFE--CTLSADALLOEFIDKROGTADDIQTVACNKMVANWTDG 280
QY 451 CDOFVAEYEPVLIEILVEVMDPSFVCLKIGACPSAHKPLLG---TEKCIWGPSYMCNTE 507
Db : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
281 CNDFVHMVYSTVLFLTYNQDGRGICTMHSCEKKENALVEMAMSEKVMLG---CEN--- 334
QY 508 TAAQCNAVEH 517
Db : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
335 ----CKAVEH 340
```

Search completed: January 13, 2006, 16:35:20
Job time : 43.6424 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 13, 2006, 16:22:54 ; Search time 199.536 Seconds
(without alignments)
1852.779 Million cell updates/sec

Title: US-10-801-517-1

Perfect score: 2789

Sequence: 1 MYALFILASLLGALAGPVL.....NTTAAQCNAVECKRHHVWN 524

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Uniprot 05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2789	100.0	524	1	P07602 h proactiva
2	2789	100.0	524	1	Q5JG36 homo sapien
3	2785	99.9	524	2	Q53FJ5 homo sapien
4	2783	99.8	529	2	Q5JQ37 homo sapien
5	2777.5	99.6	530	2	Q59EN5 HUMAN
6	2776.5	99.6	527	2	Q5NVD5 PONGY
7	2770	99.3	526	2	Q5R4U7 PONGY
8	2451.5	87.9	497	2	Q4R590 MACFA
9	2425.5	87.0	525	1	SAP BOVIN
10	2374.5	85.1	452	2	Q5R406 PONGY
11	1996	71.6	554	1	SAP RAT
12	1982.5	71.1	553	2	Q6P7A4 RAT
13	1950	69.9	554	2	Q8BFQ1 m mus muscu
14	1938.5	69.5	557	1	SAP MOUSE
15	1679.5	60.2	518	1	SAP CHICK
16	1442	51.7	512	2	Q7S770 XENLA
17	1429	51.2	518	2	Q64286 XENLA
18	1416	50.8	520	2	Q4RQ38 tetraodon n
19	1414	50.7	520	2	Q8UVZ4 BRARE
20	1412	50.6	520	2	Q6PH48 BRARE
21	1411	50.6	520	2	Q6PG7 BRARE
22	1343	48.2	522	2	Q9DG82 BRARE
23	1201	43.1	543	2	Q6NUJ1 HUMAN
24	1153	41.3	240	2	Q5BJH1 homo sapien
25	1099.5	39.4	525	2	Q8C1C1 MOUSE
26	803	28.8	245	2	Q5ZL62 CHICK
27	786	28.2	449	2	Q8BUV5 MOUSE
28	772	27.7	402	2	Q8CLN0 MOUSE
29	558	20.0	253	2	Q5R848 pongo pygma
30	552	19.8	953	2	Q9Y125 drosophila
31	545	19.5	241	2	Q8N7T4 homo sapien

32	517	18.5	121	2	P79254 SHEEP	P79254 ovis aries
33	511	18.3	965	2	O15997 BOWMO	O15997 bombyx mori
34	497.5	17.8	478	2	Q7PJ67 ANOHA	Q7PJ67 anopheles g
35	479	17.2	922	2	Q5D981 SCHJA	Q5D981 schistosome
36	432.5	15.5	876	2	Q8IMH4 DROME	Q8IMH4 drosophila
37	407	14.6	533	2	Q4JHB2 TRIVA	Q4JHB2 trichomonas
38	400.5	14.4	890	2	Q7PMW6 ANOHA	Q7PMW6 anopheles g
39	393	14.1	80	1	SAP PIG	P81405 sus scrofa
40	382	13.7	377	1	PSPB MOUSE	P50405 mus musculus
41	379	13.6	376	1	PSPB RAT	P22355 rattus norv
42	378.5	13.6	613	2	Q4JM32 TRIVA	Q4JM32 trichomonas
43	377	13.5	376	2	Q6IN44 RAT	Q6IN44 rattus norv
44	349.5	12.5	378	2	O35489 CAVPO	O35489 cavia porce
45	349.5	12.5	381	1	PSPB HUMAN	P07988 homo sapien

ALIGNMENTS

RESULT 1

ID	SAP_HUMAN	STANDARD:	PRT:	524 AA.
AC	P07602; P07292; P15793; P78538; P78541; P78546; P78547; P78558;			
AC	Q6IBQ6; Q92739; Q92740; Q92741; Q92742;			
DT	01-APR-1988 (Rel. 07, Created)			
DT	01-APR-1990 (Rel. 14, Last sequence update)			
DT	13-SEP-2005 (Rel. 48, Last annotation update)			
DE	Proactivator polypeptide precursor (Contains: Saposin A (Protein A);			
DE	Saposin B-Val; Saposin B (Sphingolipid activator protein 1) (SAP-1)			
DE	(Cerebroside sulfate activator) (CSAct) (Dispersin) (Sulfatide/GM1			
DE	activator); Saposin C (Co-beta-glucosidase) (Al activator)			
DE	(Glucosylceramidase activator) (Sphingolipid activator protein 2)			
DE	(SAP-2); Saposin D (Protein C) (Component C)).			
GN	Name=PSAP;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;			
OC	Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]_TaxID=9606;			
RP	NUCLEOTIDE SEQUENCE [MRNA].			
RC	TISSUE=Liver;			
RA	MEDLINE=90129043; PubMed=2515150;			
RT	Rorman E.G., Grabowski G.A.;			
RT	"Molecular cloning of a human co-beta-glucosidase cDNA: evidence that			
RT	four sphingolipid hydrolase activator proteins are encoded by single			
RL	genes in humans and rats.";			
RL	Genomics 5:486-492(1989).			
RL	[2]			
RP	NUCLEOTIDE SEQUENCE [MRNA].			
RA	MEDLINE=89255151; PubMed=2498298;			
RT	Nakano T., Sandhoff K., Stuenkel J., Christomanou H., Suzuki K.;			
RT	"Structure of full-length cDNA coding for sulfatide activator, a Co-			
RT	beta-glucosidase and two other homologous proteins: two alternate			
RT	forms of the sulfatide activator.";			
RL	J. Biochem. 105:152-154(1989).			
RL	[3]			
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].			
RA	Ebert L., Schick M., Neubert P., Schatten R., Henze S., Korn B.;			
RT	"Cloning of human full open reading frames in Gateway(TM) system entry			
RT	vector (pDONR201).";			
RL	Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.			
RL	[4]			
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM SAP-MU-0).			
RC	TISSUE=Brain, Eye, and Skin;			
RA	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RT	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RT	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,			

- RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmitz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalley D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
- [5]
- RP NUCLEOTIDE SEQUENCE OF 14-524.
- RP MEDLINE=88321660; PubMed=2842863;
- RA O'Brien J.S., Kretz K.A., Dewji N., Wenger D.A., Esch F., Fluhrty A.L.; "Coding of two sphingolipid activator proteins (SAP-1 and SAP-2) by same genetic locus."; Science 241:1098-1101(1988).
- [6]
- RP NUCLEOTIDE SEQUENCE OF 14-524.
- RP MEDLINE=92307663; PubMed=1612590;
- RA Rorman E.G., Scheinker V., Grabowski G.A.; "Structure and evolution of the human prosaposin chromosomal gene."; Genomics 13:312-318(1992).
- [7]
- RP PROTEIN SEQUENCE OF 17-24; 165-172; 180-189 AND 298-302.
- RP MEDLINE=93311991; PubMed=8323276; DOI=10.1006/abbi.1993.1328;
- RA Hiraiwa M., O'Brien J.S., Kishimoto Y., Galdzicka M., Fluhrty A.L., Ginns E.I., Martin B.M.; "Isolation, characterization, and proteolysis of human prosaposin, the precursor of saposins (sphingolipid activator proteins)."; Arch. Biochem. Biophys. 304:110-116(1993).
- [8]
- RP PROTEIN SEQUENCE OF 17-26.
- RP TISSUE=Milk;
- RC MEDLINE=92068206; PubMed=1958198;
- RA Kondoh K., Hinenio T., Sano A., Kakimoto Y.; "Isolation and characterization of prosaposin from human milk."; Biochem. Biophys. Res. Commun. 181:286-292(1991).
- [9]
- RP NUCLEOTIDE SEQUENCE OF 59-125 AND 304-513.
- RP TISSUE=Brain;
- RC MEDLINE=91192146; PubMed=2013321; DOI=10.1016/0014-5793(91)80308-P;
- RA Holtzschmidt H., Sandhoff K., Fuerst W., Kwon H.Y., Schnabel D., Suzuki K.; "The organization of the gene for the human cerebroside sulfate activator protein."; FEBS Lett. 280:267-270(1991).
- [10]
- RP PARTIAL PROTEIN SEQUENCE OF 60-142.
- RP MEDLINE=89240739; PubMed=2717620;
- RA Morimoto S., Martin B.M., Yamamoto Y., Kretz K.A., O'Brien J.S., Kishimoto Y.; "Saposin A: second cerebroside activator protein."; Proc. Natl. Acad. Sci. U.S.A. 86:3389-3393(1989).
- [11]
- RP PROTEIN SEQUENCE OF 62-84 AND 410-431.
- RP MEDLINE=93380576; PubMed=8370464; DOI=10.1016/0014-5793(93)80908-D;
- RA Tyynela J., Palmer D.N., Baumann M., Haltia M.; "Storage of saposins A and D in infantile neuronal ceroid-lipofuscinosis."; FEBS Lett. 330:8-12(1993).
- [12]
- RP NUCLEOTIDE SEQUENCE OF 164-524.
- RP MEDLINE=88068647; PubMed=2825202;
- RA Dewji N.N., Wenger D.A., O'Brien J.S.; "Nucleotide sequence of cloned cDNA for human sphingolipid activator protein 1 precursor."; Proc. Natl. Acad. Sci. U.S.A. 84:8652-8656(1987).
- [13]
- RP NUCLEOTIDE SEQUENCE OF 195-263.
- RP MEDLINE=86130593; PubMed=2868718;
- RA Dewji N.N., Wenger D.A., Fujibayashi S., Donoviel M., Esch F., Hill P., O'Brien J.S.; "Molecular cloning of the sphingolipid activator protein-1 (SAP-1), the sulfate sulfate activator."; Biochem. Biophys. Res. Commun. 134:989-994(1986).
- [14]
- RP PROTEIN SEQUENCE OF 195-274.
- RP MEDLINE=89207118; PubMed=3242555;
- RA Kleinschmidt T., Christomanou H., Braunitzer G.; "Complete amino-acid sequence of the naturally occurring A2 activator protein for enzymic sphingomyelin degradation: identity to the sulfate activator protein (SAP-1)."; Biol. Chem. Hoppe-Seyler 369:1361-1365(1988).
- [15]
- RP PROTEIN SEQUENCE OF 195-274.
- RP TISSUE=Kidney;
- RC MEDLINE=91006165; PubMed=2209618;
- RA Furst W., Schubert J., Machleidt W., Meyer H.B., Sandhoff K.; "The complete amino-acid sequences of human ganglioside GM2 activator protein and cerebroside sulfate activator protein."; Eur. J. Biochem. 192:709-714(1990).
- [16]
- RP PROTEIN SEQUENCE OF 311-390.
- RP MEDLINE=88163077; PubMed=3442600;
- RA Kleinschmidt T., Christomanou H., Braunitzer G.; "Complete amino-acid sequence and carbohydrate content of the naturally occurring glucosylceramide activator protein (A1 activator) absent from a new human Gaucher disease variant."; Biol. Chem. Hoppe-Seyler 368:1571-1578(1987).
- [17]
- RP PARTIAL PROTEIN SEQUENCE OF 405-484.
- RP MEDLINE=89025876; PubMed=2845979;
- RA Morimoto S., Martin B.M., Kishimoto Y., O'Brien J.S.; "Saposin D: a sphingomyelinase activator."; Biochem. Biophys. Res. Commun. 156:403-410(1988).
- [18]
- RP PROTEIN SEQUENCE OF 407-484.
- RP MEDLINE=89000190; PubMed=3048308;
- RA Furst W., Machleidt W., Sandhoff K.; "The precursor of sulfate activator protein is processed to three different proteins."; Biol. Chem. Hoppe-Seyler 369:317-328(1988).
- [19]
- RP PARTIAL PROTEIN SEQUENCE (SAPOSIN B), AND STRUCTURE OF CARBOHYDRATES.
- RC TISSUE=Urine;
- RC MEDLINE=20032116; PubMed=10562467; DOI=10.1006/mgme.1999.2900;
- RA Fluhrty A.L., Lombardo C., Louis A., Stevens R.L., Whitelegge J.P., Waring A.J., To T., Fluhrty C.B., Faull K.F.; "Preparation of the cerebroside sulfate activator (CSAct or saposin B) from human urine."; Mol. Genet. Metab. 68:391-403(1999).
- [20]
- RP DISULFIDE BONDS OF SAPOSINS B AND C, AND MASS SPECTROMETRY.
- RP MEDLINE=95247790; PubMed=7730378; DOI=10.1074/jbc.270.17.9953;
- RA Vaccaro A.M., Salvioli R., Barca A., Tatti M., Ciaffoni F., Maras B., Siciliano R., Zappacosta F., Amoresano A., Pucci P.; "Structural analysis of saposin C and B. Complete localization of disulfide bridges."; J. Biol. Chem. 270:9953-9960(1995).
- [21]
- RP STRUCTURE OF CARBOHYDRATE ON ASN-215.
- RP MEDLINE=21110404; PubMed=11180632;
- RA Faull K.F., Johnson J., Kim M.J., To T., Whitelegge J.P., Stevens R.L., Fluhrty C.B., Fluhrty A.L.; "Structure of the asparagine-linked sugar chains of porcine kidney and human urine cerebroside sulfate activator protein."; J. Mass Spectrom. 35:1416-1424(2000).
- [22]
- RP SAPOSIN D DISULFIDE BONDS.
- RP MEDLINE=99337688; PubMed=10406958;
- RA Tatti M., Salvioli R., Ciaffoni F., Pucci P., Andolfo A.,

RA Anoresano A., Vaccaro A.M.;
RT "Structural and membrane-binding properties of saposin D.";

Query Match 100.0%; Score 2789; DB 1; Length 524;
Best Local Similarity 100.0%; Pred. No. 1.3e-173;
Matches 524; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYALFLLASLLGAALAGPVLGLKECTRGSAVQCNVKTASDCGAVKHCLQTVNKPVTYS 60
DB 1 MYALFLLASLLGAALAGPVLGLKECTRGSAVQCNVKTASDCGAVKHCLQTVNKPVTYS 60

QY 61 LPDCICKDVVTAAGDMLKDNATEEELVLEKTCDWLPKPNMSASCKEIVDSYLPVILDI 120
DB 61 LPDCICKDVVTAAGDMLKDNATEEELVLEKTCDWLPKPNMSASCKEIVDSYLPVILDI 120

QY 121 IKGEMSRPGEVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVAVPFMANIFLLY 180
DB 121 IKGEMSRPGEVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVAVPFMANIFLLY 180

QY 181 PDGPRSKPQKONGDVQCDCIQMTVDIQTAVRTNSTFVQALVEHVKECDRLGPGMADI 240
DB 181 PDGPRSKPQKONGDVQCDCIQMTVDIQTAVRTNSTFVQALVEHVKECDRLGPGMADI 240

QY 241 CKNYISQYSEIAIQMMHMQPKIEICALVGFCDVEKEMPQTLVPAKVASKNVI PALELVE 300
DB 241 CKNYISQYSEIAIQMMHMQPKIEICALVGFCDVEKEMPQTLVPAKVASKNVI PALELVE 300

QY 301 PIKGEVPAKSDVYCEVCFVKEVTKLIDNNKTEKEILDADFDMCKSKLPKSLSEECQEV 360
DB 301 PIKGEVPAKSDVYCEVCFVKEVTKLIDNNKTEKEILDADFDMCKSKLPKSLSEECQEV 360

QY 361 VDTYSSILSILLEEVSPELVCSMLHLCSTRLPALTVHVTQPKDGGFCEVCKLGVYLD 420
DB 361 VDTYSSILSILLEEVSPELVCSMLHLCSTRLPALTVHVTQPKDGGFCEVCKLGVYLD 420

QY 421 RNLEKNSTQKIELAALKEGCSFLPDYPYQKQCFVAEYEPVLEILVEVMDPSFVCLKITG 480
DB 421 RNLEKNSTQKIELAALKEGCSFLPDYPYQKQCFVAEYEPVLEILVEVMDPSFVCLKITG 480

QY 481 ACPSAHKPLLGTEKICWGPSYWCNTETAACNAVEHCKRHVYN 524
DB 481 ACPSAHKPLLGTEKICWGPSYWCNTETAACNAVEHCKRHVYN 524

RESULT 2
Q5JQ36 HUMAN
ID Q5JQ36 HUMAN PRELIMINARY; PRT; 524 AA.
AC Q5JQ36;
DT 10-WAY-2005 (TrEMBLrel. 30, Created)
DT 10-WAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Proasposin (Variant Gaucher disease and variant metachromatic leukodystrophy).
GN Name=PSAP; ORFNames=RP11-472K8.1-001;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Heath P.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Kalnine N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
RA Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y.,
RA Phelan M., Farmer A.;
RT "Cloning of human full-length CDSs in BD Creator(TM) System Donor vector.";
RT Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
RL EMBL; AL731541; CAI40837.1; -; Genomic_DNA.
DR EMBL; BT006849; AAP35495.1; -; mRNA.

DR EMBL; AC073370; CAI40837.1; JOINED; Genomic_DNA.
DR GO; GO:0005764; C:lysosome; IEA.
DR GO; GO:0006629; P:lipid metabolism; IEA.
DR GO; GO:0006665; P:sphingolipid metabolism; IEA.
SQ SEQUENCE 524 AA, 58112 MW, 71977P7A8C9B1533 CRC64;

Query Match 100.0%; Score 2789; DB 2; Length 524;
Best Local Similarity 100.0%; Pred. No. 1.3e-173;
Matches 524; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYALFLLASLLGAALAGPVLGLKECTRGSAVQCNVKTASDCGAVKHCLQTVNKPVTYS 60
DB 1 MYALFLLASLLGAALAGPVLGLKECTRGSAVQCNVKTASDCGAVKHCLQTVNKPVTYS 60

QY 61 LPDCICKDVVTAAGDMLKDNATEEELVLEKTCDWLPKPNMSASCKEIVDSYLPVILDI 120
DB 61 LPDCICKDVVTAAGDMLKDNATEEELVLEKTCDWLPKPNMSASCKEIVDSYLPVILDI 120

QY 121 IKGEMSRPGEVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVAVPFMANIFLLY 180
DB 121 IKGEMSRPGEVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVAVPFMANIFLLY 180

QY 181 PDGPRSKPQKONGDVQCDCIQMTVDIQTAVRTNSTFVQALVEHVKECDRLGPGMADI 240
DB 181 PDGPRSKPQKONGDVQCDCIQMTVDIQTAVRTNSTFVQALVEHVKECDRLGPGMADI 240

QY 241 CKNYISQYSEIAIQMMHMQPKIEICALVGFCDVEKEMPQTLVPAKVASKNVI PALELVE 300
DB 241 CKNYISQYSEIAIQMMHMQPKIEICALVGFCDVEKEMPQTLVPAKVASKNVI PALELVE 300

QY 301 PIKGEVPAKSDVYCEVCFVKEVTKLIDNNKTEKEILDADFDMCKSKLPKSLSEECQEV 360
DB 301 PIKGEVPAKSDVYCEVCFVKEVTKLIDNNKTEKEILDADFDMCKSKLPKSLSEECQEV 360

QY 361 VDTYSSILSILLEEVSPELVCSMLHLCSTRLPALTVHVTQPKDGGFCEVCKLGVYLD 420
DB 361 VDTYSSILSILLEEVSPELVCSMLHLCSTRLPALTVHVTQPKDGGFCEVCKLGVYLD 420

QY 421 RNLEKNSTQKIELAALKEGCSFLPDYPYQKQCFVAEYEPVLEILVEVMDPSFVCLKITG 480
DB 421 RNLEKNSTQKIELAALKEGCSFLPDYPYQKQCFVAEYEPVLEILVEVMDPSFVCLKITG 480

QY 481 ACPSAHKPLLGTEKICWGPSYWCNTETAACNAVEHCKRHVYN 524
DB 481 ACPSAHKPLLGTEKICWGPSYWCNTETAACNAVEHCKRHVYN 524

RESULT 3
Q53FJ5 HUMAN
ID Q53FJ5 HUMAN PRELIMINARY; PRT; 524 AA.
AC Q53FJ5;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Proasposin (Variant Gaucher disease and variant metachromatic leukodystrophy) variant (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Synovial membrane;
RA Maruyama K., Sugano S.;
RT "Oligo-capping: a simple method to replace the cap structure of eucaryotic mRNAs with oligoribonucleotides.";
RL Gene 138:171-174 (1994).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Synovial membrane;
RA Suzuki Y., Yoshitomo K., Maruyama K., Sugano A., Sugano S.;
RT "Construction and characterization of a full length-enriched and a 5'-

Wed Jan 18 11:58:41 2006

```

end-enriched cDNA library." ;
Gene 200:149-156(1997).
[3]
NUCLEOTIDE SEQUENCE.
TISSUE=Synovial membrane;
Suzuki Y., Sugano S., Totoki Y., Toyoda A., Takeda T., Sakaki Y.,
Tanaka A., Yokoyama S.;
RA Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
RL EMBL; AK223290; BAD97010.1; -, mRNA.
FT NON TER 1
SQ SEQUENCE 524 AA; 58140 MW; 7034F0C71C2226BC CRC64;

Query Match 99.9%; Score 2785; DB 2; Length 524;
Best Local Similarity 99.8%; Pred. No. 2.3e-173;
Matches 523; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYALFLLASLGAALAGPVLGLKCTRGSAVWCONVKTASDCGAVKHCLQTVWNKPTVKS 60
Db 1 MYALFLLASLGAALAGPVLGLKCTRGSAVWCONVKTASDCGAVKHCLQTVWNKPTVKS 60
QY 61 LPCDICKDVVTAAGDMLKONATEBEIILVLEKTCMDLPKNMSASCKEIVDSYLPVILDI 120
Db 61 LPCDICKDVVTAAGDMLKONATEBEIILVLEKTCMDLPKNMSASCKEIVDSYLPVILDI 120
QY 61 LPCDICKDVVTAAGDMLKONATEBEIILVLEKTCMDLPKNMSASCKEIVDSYLPVILDI 120
Db 61 LPCDICKDVVTAAGDMLKONATEBEIILVLEKTCMDLPKNMSASCKEIVDSYLPVILDI 120
QY 121 IKGMSRPGVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVVAPPMANIPILLY 180
Db 121 IKGMSRPGVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVVAPPMANIPILLY 180
QY 181 PQDGRSPKQPKDNGDVQCDCIQMVTDIQTAVRTNSTFVQALVEHVKECDRLGFGMADI 240
Db 181 PQDGRSPKQPKDNGDVQCDCIQMVTDIQTAVRTNSTFVQALVEHVKECDRLGFGMADI 240
QY 241 CKNYISQYSEIAIQMMHMQPKBEICALVGFCDVEKEMPQMTLVPAKASKNVPALVELVE 300
Db 241 CKNYISQYSEIAIQMMHMQPKBEICALVGFCDVEKEMPQMTLVPAKASKNVPALVELVE 300
QY 301 PIKGEVPAKSDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDKMCCKLPSLSSECEQEV 360
Db 301 PIKGEVPAKSDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDKMCCKLPSLSSECEQEV 360
QY 361 VDTYSSILSILLEEVSPELVCSMLHLCSTGLPALTVHVTQPKDGGFCEVCCKLVGYLD 420
Db 361 VDTYSSILSILLEEVSPELVCSMLHLCSTGLPALTVHVTQPKDGGFCEVCCKLVGYLD 420
QY 421 RNLEKNSTQEIILAALEKGCFLPDYQKQCFVAEYEPVLIIEILVEVMDPSFVCLKIG 480
Db 421 RNLEKNSTQEIILAALEKGCFLPDYQKQCFVAEYEPVLIIEILVEVMDPSFVCLKIG 480
QY 481 ACPSAHKPLLGTEKCIWGPSYWCNTETAAQCNVACHKRVWN 524
Db 481 ACPSAHKPLLGTEKCIWGPSYWCNTETAAQCNVACHKRVWN 524

RESULT 4
Q5JQ37 HUMAN PRELIMINARY; PRT; 559 AA.
ID Q5JQ37;
AC Q5JQ37;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Prosaposin (Variant Gaucher disease and variant metachromatic
DE leukodystrophy).
GN Name=PSAP; ORFNames=RP11-472K9.1-002;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Heath P.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL731541; CAI40836.1; -, Genomic_DNA.

end-enriched cDNA library." ;
Gene 200:149-156(1997).
[3]
NUCLEOTIDE SEQUENCE.
TISSUE=Synovial membrane;
Suzuki Y., Sugano S., Totoki Y., Toyoda A., Takeda T., Sakaki Y.,
Tanaka A., Yokoyama S.;
RA Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
RL EMBL; AK223290; BAD97010.1; -, mRNA.
FT NON TER 1
SQ SEQUENCE 524 AA; 58140 MW; 7034F0C71C2226BC CRC64;

Query Match 99.9%; Score 2785; DB 2; Length 524;
Best Local Similarity 99.8%; Pred. No. 2.3e-173;
Matches 523; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYALFLLASLGAALAGPVLGLKCTRGSAVWCONVKTASDCGAVKHCLQTVWNKPTVKS 60
Db 1 MYALFLLASLGAALAGPVLGLKCTRGSAVWCONVKTASDCGAVKHCLQTVWNKPTVKS 60
QY 61 LPCDICKDVVTAAGDMLKONATEBEIILVLEKTCMDLPKNMSASCKEIVDSYLPVILDI 120
Db 61 LPCDICKDVVTAAGDMLKONATEBEIILVLEKTCMDLPKNMSASCKEIVDSYLPVILDI 120
QY 61 LPCDICKDVVTAAGDMLKONATEBEIILVLEKTCMDLPKNMSASCKEIVDSYLPVILDI 120
Db 61 LPCDICKDVVTAAGDMLKONATEBEIILVLEKTCMDLPKNMSASCKEIVDSYLPVILDI 120
QY 121 IKGMSRPGVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVVAPPMANIPILLY 180
Db 121 IKGMSRPGVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVVAPPMANIPILLY 180
QY 181 PQDGRSPKQPKDNGDVQCDCIQMVTDIQTAVRTNSTFVQALVEHVKECDRLGFGMADI 240
Db 181 PQDGRSPKQPKDNGDVQCDCIQMVTDIQTAVRTNSTFVQALVEHVKECDRLGFGMADI 240
QY 241 CKNYISQYSEIAIQMMHMQPKBEICALVGFCDVEKEMPQMTLVPAKASKNVPALVELVE 300
Db 241 CKNYISQYSEIAIQMMHMQPKBEICALVGFCDVEKEMPQMTLVPAKASKNVPALVELVE 300
QY 301 PIKGEVPAKSDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDKMCCKLPSLSSECEQEV 360
Db 301 PIKGEVPAKSDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDKMCCKLPSLSSECEQEV 360
QY 361 VDTYSSILSILLEEVSPELVCSMLHLCSTGLPALTVHVTQPKDGGFCEVCCKLVGYLD 420
Db 361 VDTYSSILSILLEEVSPELVCSMLHLCSTGLPALTVHVTQPKDGGFCEVCCKLVGYLD 420
QY 421 RNLEKNSTQEIILAALEKGCFLPDYQKQCFVAEYEPVLIIEILVEVMDPSFVCLKIG 480
Db 421 RNLEKNSTQEIILAALEKGCFLPDYQKQCFVAEYEPVLIIEILVEVMDPSFVCLKIG 480
QY 481 ACPSAHKPLLGTEKCIWGPSYWCNTETAAQCNVACHKRVWN 524
Db 481 ACPSAHKPLLGTEKCIWGPSYWCNTETAAQCNVACHKRVWN 524

RESULT 5
Q59S5 HUMAN PRELIMINARY; PRT; 530 AA.
ID Q59S5;
AC Q59S5;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Prosaposin variant (Fragment).
GN Name=prosaposin variant;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.

```



```
OX NCB1_TaxID=9606;
RN NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RA Totoki Y., Toyoda A., Takeda T., Sakaki Y., Tanaka A., Yokoyama S.,
RA Ohara O., Nagase T., Kikuno F.R.;
RT "None Title.";
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
FT EMBL; AB209776; BAD93013.1; -; mRNA.
FT NON TER
FT
SQ SEQUENCE 530 AA; 58727 MW; 6CA1F0159B182BC9 CRC64;

Query Match          99.6%; Score 2777.5; DB 2; Length 530;
Best Local Similarity 99.4%; Pred. No. 7.2e-173;
Matches 524; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

Qy 1 MYALFLLASLLGALAGPVGLKCTRGSAVWCNQVKTASDCGAVKHCLQTWNKPTVKS 60
Db 4 MYALFLLASLLGALAGPVGLKCTRGSAVWCNQVKTASDCGAVKHCLQTWNKPTVKS 63
Qy 61 LPCDICKDVVTAAGDMLKDNATEEELVLYLEKTCDWLPKPNMSASCKEIVDSYLPVLDI 120
Db 64 LPCDICKDVVTAAGDMLKDNATEEELVLYLEKTCDWLPKPNMSASCKEIVDSYLPVLDI 123
Qy 121 IKGMSRPGVCSALNLCESLQKHLAEINHQKLESNKIPELDMTEVVAFFMANIPILLY 180
Db 124 IKGMSRPGVCSALNLCESLQKHLAEINHQKLESNKIPELDMTEVVAFFMANIPILLY 183
Qy 181 PQDGRSKPQPKONGDVQCDCIQMVTDIQTAVRTNSTFVQALVEHVKEECDRGLPGMADI 240
Db 184 PQDGRSKPQPKONGDVQCDCIQMVTDIQTAVRTNSTFVQALVEHVKEECDRGLPGMADI 243
Qy 241 CKNYISQYSIAIQMMHMH--OPKEICALVGFCDEVKEMPOTLVPAKASKNVIPALE 297
Db 244 CKNYISQYSIAIQMMHMHQDQOPKEICALVGFCDEVKEMPOTLVPAKASKNVIPALE 303
Qy 298 LVPEPIKKEHVPAKSDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDMCKSKLPKSLSEEC 357
Db 304 LVPEPIKKEHVPAKSDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDMCKSKLPKSLSEEC 363
Qy 358 QEVVDYTGSSILSILLESVPVCSMLHLCSGTRLPALTTHVTQPKDGGFCVCKKLVG 417
Db 364 QEVVDYTGSSILSILLESVPVCSMLHLCSGTRLPALTTHVTQPKDGGFCVCKKLVG 423
Qy 418 YLDRLNLEKSTKQEIILAALEKGCSPDPYQKQCDQFVAEYEPVLIIEILVEVMDPSVCL 477
Db 424 YLDRLNLEKSTKQEIILAALEKGCSPDPYQKQCDQFVAEYEPVLIIEILVEVMDPSVCL 483
Qy 478 KIGACPSAHKPLLGTEKICWGPSYWCNTETAACNAVEHCKRHVN 524
Db 484 KIGACPSAHKPLLGTEKICWGPSYWCNTETAACNAVEHCKRHVN 530

RESULT 6
Q5NVD5_PONPY PRELIMINARY; PRT; 527 AA.
ID Q5NVD5_PONPY PRELIMINARY; PRT; 526 AA.
AC Q5NVD5;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Hypothetical protein DKFp459F0110.
GN Name=DKFp459F0110;
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;
OC Pongo.
OX NCB1_TaxID=9606;
RN NUCLEOTIDE SEQUENCE.
RC TISSUE=Cortex;
RG The German cDNA Consortium;
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Pobo G., Han M., Wiemann S.;
```

```
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR296102; CA129728.1; -; mRNA.
DR SNR; Q5NVD5; 194-275, 314-393.
DR GO; GO:0005764; C:lysosome; IEA.
DR GO; GO:0006629; P:lipid metabolism; IEA.
DR GO; GO:0006665; P:sphingolipid metabolism; IEA.
DR InterPro; IPR003119; Sapa.
DR InterPro; IPR007856; SapaB.1.
DR InterPro; IPR008138; SapaB.2.
DR InterPro; IPR008140; SapaB_sub.
DR InterPro; IPR008373; Saposin.
DR InterPro; IPR008139; SaposinB.
DR Pfam; PF02199; Sapa; 2.
DR Pfam; PF05184; SapaB.1; 4.
DR Pfam; PF03489; SapaB.2; 4.
DR PRINTS; PR01797; SAPOSIN.
DR ProDom; PD001732; SapaB_sub.2.
DR SMART; SM00162; SAPA; 2.
DR Hypothetical protein.
SQ SEQUENCE 527 AA; 58469 MW; 293FBB746C29C4D0 CRC64;

Query Match          99.6%; Score 2776.5; DB 2; Length 527;
Best Local Similarity 99.2%; Pred. No. 8.3e-173;
Matches 523; Conservative 1; Mismatches 0; Indels 3; Gaps 1;

Qy 1 MYALFLLASLLGALAGPVGLKCTRGSAVWCNQVKTASDCGAVKHCLQTWNKPTVKS 60
Db 1 MYALFLLASLLGALAGPVGLKCTRGSAVWCNQVKTASDCGAVKHCLQTWNKPTVKS 60
Qy 61 LPCDICKDVVTAAGDMLKDNATEEELVLYLEKTCDWLPKPNMSASCKEIVDSYLPVLDI 120
Db 61 LPCDICKDVVTAAGDMLKDNATEEELVLYLEKTCDWLPKPNMSASCKEIVDSYLPVLDI 120
Qy 121 IKGMSRPGVCSALNLCESLQKHLAEINHQKLESNKIPELDMTEVVAFFMANIPILLY 180
Db 121 IKGMSRPGVCSALNLCESLQKHLAEINHQKLESNKIPELDMTEVVAFFMANIPILLY 180
Qy 181 PQDGRSKPQPKONGDVQCDCIQMVTDIQTAVRTNSTFVQALVEHVKEECDRGLPGMADI 240
Db 181 PQDGRSKPQPKONGDVQCDCIQMVTDIQTAVRTNSTFVQALVEHVKEECDRGLPGMADI 240
Qy 241 CKNYISQYSIAIQMMHMH--OPKEICALVGFCDEVKEMPOTLVPAKASKNVIPALE 297
Db 241 CKNYISQYSIAIQMMHMHQDQOPKEICALVGFCDEVKEMPOTLVPAKASKNVIPALE 300
Qy 298 LVPEPIKKEHVPAKSDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDMCKSKLPKSLSEEC 357
Db 301 LVPEPIKKEHVPAKSDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDMCKSKLPKSLSEEC 360
Qy 358 QEVVDYTGSSILSILLESVPVCSMLHLCSGTRLPALTTHVTQPKDGGFCVCKKLVG 417
Db 361 QEVVDYTGSSILSILLESVPVCSMLHLCSGTRLPALTTHVTQPKDGGFCVCKKLVG 420
Qy 418 YLDRLNLEKSTKQEIILAALEKGCSPDPYQKQCDQFVAEYEPVLIIEILVEVMDPSVCL 477
Db 421 YLDRLNLEKSTKQEIILAALEKGCSPDPYQKQCDQFVAEYEPVLIIEILVEVMDPSVCL 480
Qy 478 KIGACPSAHKPLLGTEKICWGPSYWCNTETAACNAVEHCKRHVN 524
Db 481 KIGACPSAHKPLLGTEKICWGPSYWCNTETAACNAVEHCKRHVN 527

RESULT 7
Q5R4U7_PONPY PRELIMINARY; PRT; 526 AA.
ID Q5R4U7_PONPY PRELIMINARY; PRT; 526 AA.
AC Q5R4U7;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Hypothetical protein DKFp459J1314.
GN Name=DKFp459J1314;
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;
OC Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Cortex;
RG The German cDNA Consortium;
RA Bloeker H., Boecker H., Brandt P., Mewes H.W., Weil B., Amid C.,
RA Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR861144; CAH93219.1; -; mRNA.
DR SMR; Q8407; 194-274, 313-392.
DR GO; GO:0005764; C:lysosome; IEA.
DR GO; GO:0006629; P:lipid metabolism; IEA.
DR GO; GO:0006665; P:sphingolipid metabolism; IEA.
DR InterPro; IPR003119; Sapa.
DR InterPro; IPR007856; SapB_1.
DR InterPro; IPR008138; SapB_2.
DR InterPro; IPR008140; SapB_sub.
DR InterPro; IPR008373; Saposin.
DR InterPro; IPR008139; SaposinB.
DR Pfam; PF02199; Sapa; 2.
DR Pfam; PF05184; SapB_1; 4.
DR Pfam; PF03489; SapB_2; 4.
DR PRINTS; PR01797; SAPOSIN.
DR ProDom; PD001732; SapB_sub; 2.
DR SMART; SM00162; SAPA; 2.
KW Hypothetical protein.
SQ SEQUENCE 526 AA; 58325 MW; CF3B146DDB6F5539 CRC64;

Query Match 99.3%; Score 2770; DB 2; Length 526;
Best Local Similarity 99.2%; Pred. No. 2.2e-172;
Matches 522; Conservative 1; Mismatches 1; Indels 2; Gaps 1;

QY 1 MYALFLASLLGNAALAGPVLGKCTRGSAVWCNQVKTASDCGAVKHCLQTVWNKPTVKS 60
DB 1 MYALFLASLLGNAALAGPVLGKCTRGSAVWCNQVKTASDCGAVKHCLQTVWNKPTVKS 60

QY 61 LPDCICKDVVTAAGDMLKDNATEEBEILVLEKTCDWLPKPNNSASCKEIVDSYLPVLDI 120
DB 61 LPDCICKDVVTAAGDMLKDNATEEBEILVLEKTCDWLPKPNNSASCKEIVDSYLPVLDI 120

QY 121 IKGMSRPGEVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVVAFFMANIPLLLY 180
DB 121 IKGMSRPGEVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVVAFFMANIPLLLY 180

QY 181 PDGPRSKPQPKDNGDVQCDCIQMVTDIQTAVRTNSTFVQALVEHVKECDRLGPGMADI 240
DB 181 PDGPRSKPQPKDNGDVQCDCIQMVTDIQTAVRTNSTFVQALVEHVKECDRLGPGMADI 240

QY 241 CKNYISQYSEIAIQMMHMH- - - QPKETCALVGFCDVEKEMPQTLVPAKVASKNVI PALEL 298
DB 241 CKNYISQYSEIAIQMMHMHQDQPKETCALVGFCDVEKEMPQTLVPAKVASKNVI PALEL 300

QY 299 VEPFKKHEVPKSDVYCEVCEFLVKEVTKLIDNNKTEKELIDAFDMCKSLPKSISEEQ 358
DB 301 VEPFKKHEVPKSDVYCEVCEFLVKEVTKLIDNNKTEKELIDAFDMCKSLPKSISEEQ 360

QY 359 EVVDTYGSISLILLESPELVCSMLHLCSTGRLPALTVHTVTPQKGGFCVCKLVGY 418
DB 361 EVVDTYGSISLILLESPELVCSMLHLCSTGRLPALTVHTVTPQKGGFCVCKLVGY 420

QY 419 LDRNLKNSYKQIBLAALAEKGSFLPDYQKQCDQFVAEYEPVLIILVEVMDPSFVCLK 478
DB 421 LDRNLKNSYKQIBLAALAEKGSFLPDYQKQCDQFVAEYEPVLIILVEVMDPSFVCLK 480

QY 479 IGACPSAHKPLLTGTEKCIWGPSYWCQNTETAAQCNAVEHCKRHVN 524
DB 481 IGACPSAHKPLLTGTEKCIWGPSYWCQNTETAAQCNAVEHCKRHVN 526

RESULT 8
Q4R590_MACFA

ID Q4R590 MACFA PRELIMINARY; PRT; 497 AA.
AC Q4R590;
DT 13-SEP-2005 (TReMBLrel. 31, Created)
DT 13-SEP-2005 (TReMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TReMBLrel. 31, Last annotation update)
DE Brain cDNA, clone: QccE-13090, similar to human prosaposin (variant
DE Gaucher disease and variantmetachromatic leukodystrophy) (PSAP),
DE Brain cDNA, clone: QccE-13989, similar to human prosaposin (variant
DE Gaucher disease and variantmetachromatic leukodystrophy)
DE (PSAP)).
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopitheidae; Cercopithecinæ; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA International consortium for macaque cDNA sequencing, analysis;
RT "DNA sequences of macaque genes expressed in brain or testis and its
RT evolutionary implications.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Osada N., Hitata M., Tanuma R., Kusuda J., Hida M., Suzuki Y.,
RA Sugano S., Gojobori T., Shen J.C.-K., Wu C.I., Hashimoto K.;
RT "Substitution rate and structural divergence of 5'UTR evolution;
RT Comparative analysis between human and cynomolgus monkey cDNAs";
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB169654; BAB01735.1; -; mRNA.
DR EMBL; AB169527; BAB01609.1; -; mRNA.
SQ SEQUENCE 497 AA; 55306 MW; 4A1974F8DB883900 CRC64;

Query Match 87.9%; Score 2451.5; DB 2; Length 497;
Best Local Similarity 97.9%; Pred. No. 1.3e-151;
Matches 468; Conservative 3; Mismatches 4; Indels 3; Gaps 1;

QY 1 MYALFLASLLGNAALAGPVLGKCTRGSAVWCNQVKTASDCGAVKHCLQTVWNKPTVKS 60
DB 1 MYALFLASLLGNAALAGPVLGKCTRGSAVWCNQVKTASDCGAVKHCLQTVWNKPTVKS 60

QY 61 LPDCICKDVVTAAGDMLKDNATEEBEILVLEKTCDWLPKPNNSASCKEIVDSYLPVLDI 120
DB 61 LPDCICKDVVTAAGDMLKDNATEEBEILVLEKTCDWLPKPNNSASCKEIVDSYLPVLDI 120

QY 121 IKGMSRPGEVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVVAFFMANIPLLLY 180
DB 121 IKGMSRPGEVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVVAFFMANIPLLLY 180

QY 181 PDGPRSKPQPKDNGDVQCDCIQMVTDIQTAVRTNSTFVQALVEHVKECDRLGPGMADI 240
DB 181 PDGPRSKPQPKDNGDVQCDCIQMVTDIQTAVRTNSTFVQALVEHVKECDRLGPGMADI 240

QY 241 CKNYISQYSEIAIQMMHMH- - - QPKETCALVGFCDVEKEMPQTLVPAKVASKNVI PALE 297
DB 241 CKNYISQYSEIAIQMMHMHQDQPKETCALVGFCDVEKEMPQTLVPAKVASKNVI PALE 300

QY 298 VEPFKKHEVPKSDVYCEVCEFLVKEVTKLIDNNKTEKELIDAFDMCKSLPKSISEEC 357
DB 301 VEPFKKHEVPKSDVYCEVCEFLVKEVTKLIDNNKTEKELIDAFDMCKSLPKSISEEC 360

QY 358 QEVVDTYGSISLILLESPELVCSMLHLCSTGRLPALTVHTVTPQKGGFCVCKLVGY 417
DB 361 QEVVDTYGSISLILLESPELVCSMLHLCSTGRLPALTVHTVTPQKGGFCVCKLVGY 420

QY 418 YLDRNLKNSYKQIBLAALAEKGSFLPDYQKQCDQFVAEYEPVLIILVEVMDPSFV 475
DB 421 YLDRNLKNSYKQIBLAALAEKGSFLPDYQKQCDQFVAEYEPVLIILVEVMDPSFV 478

RESULT 9
SAP_BOVIN
ID - SAP_BOVIN STANDARD; PRT; 525 AA.
AC P26779; Q9N2G4;

Db	241	MCKNYINQYSEVAIQVMHMQPKEICVLAFGFCDEVKEMPMTKTLVPAEYVSENVPALGLV	300
Qy	300	EPKKHVEPAKSDVYCEVCEFLVKEVTKLIDNNKTEKEILDAFKMCKSLPKSLSEECQE	359
Db	301	EPKKHVEPAKSDVYCEVCEFLVKEVTKLIDNNKTEKEILDAFKMCKSLPKSLSEECQE	360
Qy	360	VVDYTGSSILILAEVSPVLCVSMHLCSGTRLPALTVHVTQPKDGGFCVCKKLVGYL	419
Db	361	VVDYTGSSILILAEVSPVLCVSMHLCSGTRLPALTVHVTQPKDGGFCVCKKLVGYL	420
Qy	420	DRNLEKSTKQEIILAEKGCSEFLPDPYQKQCDQFVAEYEPVLIEILVEMDPSFVCLKI	479
Db	421	DRNLEKSTKQEIILAEKGCSEFLPDPYQKQCDQFVAEYEPVLIEILVEMDPSFVCLKI	480
Qy	480	GACPSAHKPLGTEKICNGPSPYWCNTETAACQNAVEHCKRHVMN	524
Db	481	GACPSAHKPLGTEKICNGPSPYWCNTETAACQNAVEHCKRHVMN	525
RESULT 10			
Qy	Q5R406	PONPY PRELIMINARY; PRT; 452 AA.	
AC	Q5R406		
DT	01-FEB-2005	(Tremblrel. 29, Created)	
DT	01-FEB-2005	(Tremblrel. 29, Last sequence update)	
DT	01-FEB-2005	(Tremblrel. 29, Last annotation update)	
DE	Hypothetical protein DKFZp459G152.		
GN	Name=DKFZp459G152;		
OS	Pongo pygmaeus (Orangutan).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;		
OC	Pongo.		
OX	NCBI_TaxID=9600;		
RN	[1]		
RP	NUCLEOTIDE SEQUENCE.		
RC	TISSUE=Cortex;		
RG	The German cDNA Consortium;		
RA	Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,		
RA	Fobo G., Han M., Wienann S.;		
RL	Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; CR861454; CAH93510.1; -; mRNA.		
DR	SMR; Q5R406; 119-200, 239-318.		
DR	GO; GO:0005764; C:lysosome; IEA.		
DR	GO; GO:0006629; P:lipid metabolism; IEA.		
DR	GO; GO:0006665; P:sphingolipid metabolism; IEA.		
DR	InterPro; IPR003119; Sapa.		
DR	InterPro; IPR007856; Sapa 1.		
DR	InterPro; IPR008138; Sapa 2.		
DR	InterPro; IPR008140; Sapa sub.		
DR	InterPro; IPR008373; Saposin.		
DR	InterPro; IPR008139; SaposinB.		
DR	Pfam; PF02199; Sapa; 1.		
DR	Pfam; PF05184; Sapa 1; 4.		
DR	Pfam; PF03489; Sapa 2; 4.		
DR	PRINTS; PR01797; SAPOSIN.		
DR	ProDom; PD001732; Sapa sub; 2.		
DR	SMART; SM00162; SAPA; 1.		
KW	Hypothetical protein.		
SQ	SEQUENCE 452 AA; 50664 MW; 6D30EAC665A399DD CRC64;		
Query Match 85.1%; Score 2374.5; DB 2; Length 452;			
Best Local Similarity 99.1%; Pred. No. 1-2e-146;			
Matches 448; Conservative 1; Mismatches 0; Indels 3; Gaps 1;			
Qy	76	MLKDNATEEILVYLEKTCDWLPKPNMSCKEIVDSYLPVILDIKNGSRGFEVCSAL	135
Db	1	MLKDNATEEILVYLEKTCDWLPKPNMSCKEIVDSYLPVILDIKNGSRGFEVCSAL	60
Qy	136	NLCESLQKHLAEHLNHOLESNKIPELDMTEVVAPEWNPILLYPDQDGRSKPQKNG	195
Db	61	NLCESLQKHLAEHLNHOLESNKIPELDMTEVVAPEWNPILLYPDQDGRSKPQKNG	120
Qy	196	DVQCDCIQMVDITQAVRTNSTFQVALVEHVEKCDRLGPGMADICKNYISQYSEIAIQM	255

```
DR EMBL; M19936; AAA42136.1; -; mRNA.
DR EMBL; S81353; AAB36042.2; -; mRNA.
DR EMBL; S81373; AAB36233.2; -; mRNA.
DR PIR; A28716; A28716.
DR HSSP; Q22739; 1N69.
DR SMR; P10960; 195-271.
DR Ensemble; ENSRNOG00000000571; Rattus norvegicus.
DR RGD; 3423; Peap.
DR GO; GO:0046836; P-glycolipid transport; NAS.
DR InterPro; IPR009007; Pept_Aspartc_cat.
DR InterPro; IPR003119; Sapa.
DR InterPro; IPR007856; SapB 1.
DR InterPro; IPR008138; SapB 2.
DR InterPro; IPR008140; SapB sub.
DR InterPro; IPR008373; Saposin.
DR InterPro; IPR008139; SaposinB.
DR Pfam; PF02199; Sapa; 2.
DR Pfam; PF05184; SapB 1; 3.
DR Pfam; PF03489; SapB 2; 4.
DR PRINTS; PR01797; SAPOSIN.
DR ProDom; PD001732; SapB sub; 1.
DR PROSITE; PS51110; SAP_A; 2.
DR PROSITE; PS50015; SAP_B; 4.
DR Direct protein sequencing; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 16
FT CHAIN 17 554 Sulfated glycoprotein 1.
FT DOMAIN 18 58 Saposin A-type 1.
FT DOMAIN 59 142 Saposin B-type 1.
FT DOMAIN 193 274 Saposin B-type 3.
FT DOMAIN 310 391 Saposin B-type 3.
FT DOMAIN 435 516 Saposin B-type 4.
FT DOMAIN 518 554 Saposin A-type 2.
FT CARBOHYD 80 80 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 214 214 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 331 331 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 456 456 N-linked (GlcNAc...) (Potential).
FT DISULFID 63 138 By similarity.
FT DISULFID 66 132 By similarity.
FT DISULFID 94 106 By similarity.
FT DISULFID 197 270 By similarity.
FT DISULFID 200 264 By similarity.
FT DISULFID 229 240 By similarity.
FT DISULFID 314 387 By similarity.
FT DISULFID 317 381 By similarity.
FT DISULFID 345 356 By similarity.
FT DISULFID 439 512 By similarity.
FT DISULFID 442 506 By similarity.
FT DISULFID 470 481 By similarity.
FT CONFLICT 115 115 P -> L (in Ref. 2 and 3).
FT CONFLICT 299 299 D -> E (in Ref. 2).
FT CONFLICT 462 462 I -> V (in Ref. 3).
FT CONFLICT 527 527 W -> R (in Ref. 3).
FT CONFLICT 536 536 S -> M (in Ref. 3).
FT SEQUENCE 554 AA; 61124 MW; DFE3F3A3A0520C6B CRC64;

Query Match
Best Local Similarity 71.68; Score 1996; DB 1; Length 554;
Matches 369; Conservative 77; Mismatches 78; Indels 32; Gaps 3;

QY 1 MYALFLIASLLGALAGPVLGLKECTRGSAVQCNVKTASDCGAVKHCLQTVVWKPTVKS 60
DB 1 MYALALLASLLVLTALTSVPQDPKICSGSAVCRVDKTAVDCAVHKCQQMWWSKPTAKS 60
QY 61 LPDCICKDVVTAAGDMLKDNATBEILVYLEKTDWLPKPNMGSACKEIVDSYLPVLDI 120
DB 61 LPDCICKVTVEAGNLKDNATBEILVYLEKTCWTHDSLSASCKEVVDSYLPVLDM 120
QY 121 IKGEMSPGVCNALNICSLOKHLAELNHQKLESNKIPELDMTEVVAFPMANIPILLY 180
DB 121 IKGEMSPGVCNALNICSLOQELAEQN-ORQLESNKIPFVDLARVVAFPMNSIPILLY 179
QY 181 PQDPRSPQPKONGDVCQDCIQMWTDIQTAVRTNSTFVQALVEHVKEECDRLGPGMADI 240
```

```
Db 180 PQDPRSPQPKANEDVQCQCKMLVTDIQTAVRTNSTSFVQGLVDHVKEDCDRLGPGVSDI 239
QY 241 CKNYISQYSEIATQMMHMQPKEICALVGFCDDEVKEMPMQTLVPAKVASKNVIPALELVE 300
Db 240 CKNYVDQYSEVAVQMMHMQPKEICVMVGFCDDEVKVPMTTLVPAEATKNIILPALELTD 299
QY 301 PIKKEHVPAKSDVYCEVCFELVKEVTKLIDNNKTEKEIILDADPMCKSKLPKSLSEBCEQV 360
Db 300 PVEQDVIQAQWIFCQVQLVMKLSLSELIINNATELLINKLSKACSLLPAPASTKCOEV 359
QY 361 VDTYSSILSILLREVSPELVCSMLHLCSSG-----TRLP----- 394
Db 360 LVTGSPSLDLVLMHEVNPFPNFCVLSCSANPNLVGTLQEPAAAIVSALPKPEAPPKQPE 419
QY 395 -----ALTVHVTPQKDGGFCEVCKKLVGYLDRLNLRKSTKQEIILAALEKGCSPFLPDYQK 449
Db 420 EPKQSALRAHVPQKNGGFCVCKKLVLYLEHNLEKSTKEEILAALEKGCSPFLPDYQK 479
QY 450 QCDQFVAEYEPVLIEILVEVMDPSFVCLKIGACPSAHKPLLGTEKINGSPSYWCONTETA 509
Db 480 QCDEFVARYEPLLEILVEVMDPSFVCSKIGVCPSPAYKLLLGTEKCVMGFGYWCNSETD 539
QY 510 ACQNAVEHCKRHVMN 524
Db 540 ARCNAVHDCKRHVMN 554

RESULT 12
Q6P7A4 RAT PRELIMINARY; PRT; 553 AA.
AC Q6P7A4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Prosaposin.
GN Name=Psap;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Prostate;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uadin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pahay J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywicki M.I., Skalska U., Smallus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Prostate;
RA Strausberg R.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC061759; AAH61759.1; -; mRNA.
DR SMR; Q6P7A4; 195-271.
DR GO; GO:0005764; C:lysosome; IEA.
```

DR GO:0006629; P:lipid metabolism; IEA.
DR GO:0006665; P:sphingolipid metabolism; IEA.
DR InterPro: IPR001119; SApA.
DR InterPro: IPR007856; SApB_1.
DR InterPro: IPR008138; SApB_2.
DR InterPro: IPR008140; SApB_sub.
DR InterPro: IPR008173; Saposin.
DR InterPro: IPR008139; SaposinB.
DR Pfam: PF02199; SApA_2.
DR Pfam: PF05184; SApB_1; 3.
DR Pfam: PF03489; SApB_2; 4.
DR PRINTS: PR01797; SAPOSIN.
DR ProDom: PD001732; SApB_sub; 1.
DR SMART: SM00162; SApA; 2.
SQ SEQUENCE 553 AA; 61039 MW; 63F3DD5E0C523393 CRC64;

Query Match 71.1%; Score 1982.5; DB 2; Length 553;
Best Local Similarity 66.3%; Pred. No. 5.7e-121;
Matches 368; Conservative 75; Mismatches 79; Indels 33; Gaps 4;

QY 1 MYALFLASLALGALAGPVLGKECTRGSAVMQVKTASDCGAVKHCLQTVNKPVTKS 60
Db 1 MYALFLASLALTATSPVQPKICSGSAVVCVRDKTAVDCRAVKHCQQWWSKPTAKS 60
QY 61 LPDCICKDVVTAAGDMLKDNATEEBEILVYLEKTDMLPKPNMSASCKEIVDSYLPVILDI 120
Db 61 LPDCICKVTVEAGLLKDNATEEBEILVYLEKTCWIKAWIHDSLSASCKEIVDSYLPVILDM 120
QY 121 IKGEMSRGCEVSALNLCESLQKLAELNHQKLESNKIPELDMTEVAVPMANIPALLY 180
Db 121 IKGEMSNRGEVSALNLCQSLQELYLAEQN-QRQLESNKIPEVDLVARVAPFMSNIPALLY 179
QY 181 PDGPRSRPQPKNGDVCDCTQMTVDITQAVRTNSTFQVALVHVHVEKEDCLRGGMADI 240
Db 180 PDQRPRSQPKANEDVCDCKMLVTDITQAVRTNSTFQGLVHVHVEKEDCLRGFGVSDI 239
QY 241 CKNYISQYSEIAIQMMHMQPKIEICALGVGFCDEVKEMPQTLVPAKVAASKNVIPALELVE 300
Db 240 CKNYVDQYSEVAVQMMHMQPKIEICVMVGFCDVKKVPMRTLVPAEAIKNILPALELTD 299
QY 301 PIKHEVPKANSVYCEVCEFLVKEVTKLIDNNKTEKELDAPDKVCKSLPKSLSECEVEV 360
Db 300 PY-EDVIOAQNVIFQVQVQLVNRKLSIELINNATEELLIKGLSKAKCSLLPAPASTKCEV 358
QY 361 VDTYGSSTLSILLESVPELVCSMLHLCSG-----TRLP----- 394
Db 359 LVTFGSLDVLVHVEVNPFLCGVISLCSANPNLVGTLTLEQPAAIIVSALPKPEAPPKQPE 418
QY 395 -----ALTVHVTPQKDGGFCEVCKKLVGLDRNLEKNSTKQBIILAALKEGCSFLPDYQK 449
Db 419 EPKQALRAHVPPQKNGGFCEVCKKLVILEHNLEKNSTKEBIILAALKEGCSFLPDYQK 478
QY 450 QCDQPVAEYEPVLIELVEMDPSFVCLKIGKACPSAHKPLLTGTEKICWPGSTWCQNTETA 509
Db 479 QCDEFVAEYEPVLIELVEMDPSFVCSKIGVCPKAYKLLGLTEKCVWVGWYQWQNMETA 538
QY 510 AQCNVAEHCKRHWVN 524
Db 539 ARCNVDVHCKRHWVN 553

RESULT 13
QB8FQ1 MOUSE
ID QB8FQ1_MOUSE PRELIMINARY; PRT; 554 AA.
AC QB8FQ1;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Mus musculus 2 days neonate thymus thymic cells cdna, RIKEN full-length enriched library, clone:E430014B12 product:proposin, full insert sequence (Mus musculus kidney CCL-142 RAG cDNA, RIKEN full-length enriched library, clone:G430050G07 product:proposin, full insert sequence).

GN OS
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NOD, and BALB/C; TISSUE=Kidney, and Thymus;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NOD, and BALB/C; TISSUE=Kidney, and Thymus;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaudo I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tonita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.P., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P., Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S., Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RN Nature 409:685-690(2001).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NOD, and BALB/C; TISSUE=Thymus, and Kidney;
RX MEDLINE=23254681; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S., Nikaudo I., Oeato N., Saito R., Suzuki H., Yamana K.I., Kiyosawa H., Yagi K., Tomaru I., Hasegawa Y., Nogi A., Hume D.A., Quackenbush J., Baldarelli R., Hill D.P., Bult C., Hume D.A., Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W., Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S., Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer J.K., Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J., Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D., Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L., Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A., Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H., Nagashima T., Numata K., Okido T., Pavan W.J., Perlea G., Pesole G., Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S., Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M., Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K., Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M., Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C., Wilming L.G., Wyshaw-Boris A., Yanagisawa M., Yang I., Yang L., Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayashizaki Y., Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K., Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S., Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I., Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A., Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J., Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NOD, and BALB/C; TISSUE=Kidney, and Thymus;

```

RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RL prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NOD, and BALB/C; TISSUE=Kidney, and Thymus;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuina T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yanamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NOD, and BALB/C; TISSUE=Kidney, and Thymus;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai K., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yaeunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK088369; BAC40308.1; -; mRNA.
DR ENBL; AK089998; BAC41035.1; -; mRNA.
DR HSSP; Q92739; IN69.
DR SMR; Q8BFQ1; 195-271.
DR MGI; MGI:197783; Peap.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0005739; C:mitochondrion; IDA.
DR InterPro; IPR003119; SapA.
DR InterPro; IPR007856; SapB 1.
DR InterPro; IPR008138; SapB 2.
DR InterPro; IPR008140; SapB_sub.
DR InterPro; IPR008373; Saposin.
DR InterPro; IPR008139; SaposinB.
DR Pfam; PF02199; SapA; 2.
DR Pfam; PF05184; SapB 1; 4.
DR Pfam; PF03489; SapB 2; 4.
DR PRINTS; PR01797; Saposin.
DR ProDom; PD001732; SapB sub; 1.
DR SMART; SM00162; SAPA; 2.
DR SMART; SM00741; SapB; 4.
SQ SEQUENCE 554 AA; 61050 MW; FF58DB79C7CC0C18 CRC64;

Query Match 69.9%; Score 1950; DB 2; Length 554;
Best Local Similarity 64.0%; Pred. No. 7.6e-119;
Matches 355; Conservative 78; Mismatches 90; Indels 32; Gaps 2;

QY 1 MYALFLASLLGALAGPVLGKCECTRGSAVMCONVKYATDCGAVKHCLOTVMKPTVKS 60
DB 1 MYALALFASLLATALTSPVDPTCKGGSAVLCDVKTAADCGAVKHCQOMWSKETAKS 60

QY 61 LPCDICKVVTAGDMLKDNATEBEELVLYLEKTCWLPKPNMSASCKEIVDSYLPVILDI 120
DB 61 LPCDICKVVTAGNLKDNATQEBEILVLYLEKTCWLIHDSLSASCKEVVDSYLPVILDM 120

QY 121 IKGEMSRPVECSALNCSLSQKHLAELNHQKLESNKIPELDMTEVVAFFWNPILPLY 180
DB 121 IKGEMSNPGEVCSALNCSLSQKLEYLAQN-QKQLESNKIPEDVMARVAPFMSNIPLLY 179

```


CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC

CC	ENBL	S36200	AAB22175.1	-	mrRNA
DR	ENBL	S71616	AAB31059.1	-	mrRNA
DR	ENBL	U27340	AAA92567.1 <th>-</th> <th>mrRNA</th>	-	mrRNA
DR	ENBL	U57999	AAB02695.1 <th>-</th> <th>Genomic_DNA</th>	-	Genomic_DNA
DR	PIR	JH0604	JH0604		
DR	HSSP	Q92739	IN69		
DR	SMR	O61207	195-274		
DR	Ensembl	ENSMUSG00000004207	Mus musculus		
DR	MGI	MGI:97783	Peap		
DR	GO	GO:0005615	C:extracellular space		TAS
DR	GO	GO:0005739	C:mitochondrion		IDA
DR	InterPro	IPR009007	Pept_Aspartc_cat		
DR	InterPro	IPR003119	SapA		
DR	InterPro	IPR007856	SapB 1		
DR	InterPro	IPR008138	SapB 2		
DR	InterPro	IPR008140	SapB_sub		
DR	InterPro	IPR008373	Saposin		
DR	InterPro	IPR008139	Saposinb		
DR	Pfam	PF02199	SapA; 2		
DR	Pfam	PF05184	SapB 1; 4		
DR	Pfam	PF03489	SapB 2; 4		
DR	PRINTS	PR01797	SAPOSIN		
DR	ProDom	PD001732	SapB_sub; 1		
DR	PROSITE	PS51110	SAP A; 2		
DR	PROSITE	PS50015	SAP B; 4		
DR	Glycoprotein	Repeat	Signal		
KW	Glycoprotein	1	16		
FT	CHAIN	17	557		By similarity.
FT	DOMAIN	18	58		Sulfated glycoprotein 1.
FT	DOMAIN	59	142		Saposin A-type 1.
FT	DOMAIN	193	277		Saposin B-type 1.
FT	DOMAIN	313	394		Saposin B-type 2.
FT	DOMAIN	438	519		Saposin B-type 3.
FT	DOMAIN	521	557		Saposin B-type 4.
FT	DOMAIN	80	80		Saposin A-type 2.
FT	CARBOHYD	214	214		N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	334	334		N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	459	459		N-linked (GlcNAc. . .) (Potential).
FT	DISULFID	63	138		By similarity.
FT	DISULFID	66	132		By similarity.
FT	DISULFID	94	106		By similarity.
FT	DISULFID	197	273		By similarity.
FT	DISULFID	200	267		By similarity.
FT	DISULFID	229	240		By similarity.
FT	DISULFID	317	390		By similarity.
FT	DISULFID	320	384		By similarity.
FT	DISULFID	348	359		By similarity.
FT	DISULFID	442	515		By similarity.
FT	DISULFID	445	509		By similarity.
FT	DISULFID	473	484		By similarity.
FT	CONFLICT	83	83		Q -> E (in Ref. 2).
FT	CONFLICT	158	158		I -> V (in Ref. 3).
FT	CONFLICT	160	160		Missing (in Ref. 2).
FT	CONFLICT	171	172		MS -> SA (in Ref. 3).
FT	CONFLICT	244	244		V -> L (in Ref. 2).
FT	CONFLICT	254	254		M -> I (in Ref. 3).
FT	CONFLICT	255	255		L -> W (in Ref. 2).
FT	CONFLICT	260	262		Missing (in Ref. 3).
FT	CONFLICT	307	307		N -> D (in Ref. 2).
FT	CONFLICT	307	307		F -> L (in Ref. 2).
FT	CONFLICT	322	322		AL -> GV (in Ref. 1).
FT	CONFLICT	349	350		G -> D (in Ref. 3).
FT	CONFLICT	367	367		L -> Q (in Ref. 2).
FT	CONFLICT	370	370		I -> D (in Ref. 3).
FT	CONFLICT	373	391		A -> T (in Ref. 3).
FT	CONFLICT	391	391		R -> L (in Ref. 3).
FT	CONFLICT	393	393		A -> R (in Ref. 2 and 3).
FT	CONFLICT	406	406		P -> R (in Ref. 2).
FT	CONFLICT	430	430		

RP NUCLEOTIDE SEQUENCE.
RA Altman N., Horowitz M.;
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: The lysosomal degradation of sphingolipids takes place
CC by the sequential action of specific hydrolases. Some of these
CC enzymes require specific low-molecular mass, non-enzymic proteins:
CC the sphingolipids activator proteins (coproteins) (By similarity).
CC -!- FUNCTION: Saposin A and saposin C stimulate the hydrolysis of
CC glucosylceramide by beta-glucosylceramidase (EC 3.2.1.45) and
CC galactosylceramide by beta-galactosylceramidase (EC 3.2.1.46).
CC Saposin C apparently acts by combining with the enzyme and acidic
CC lipid to form an activated complex, rather than by solubilizing
CC the substrate (By similarity).
CC -!- FUNCTION: Saposin B stimulates the hydrolysis of galacto-
CC cerebroside sulfate by arylsulphatase A (EC 3.1.6.8), GM1
CC gangliosides by beta-galactosidase (EC 3.2.1.23) and
CC globotriaosylceramide by alpha-galactosidase A (EC 3.2.1.22).
CC Saposin B forms a solubilizing complex with the substrates of the
CC sphingolipid hydrolases (By similarity).
CC -!- FUNCTION: Saposin D is a specific sphingomyelin phosphodiesterase
CC activator (EC 3.1.4.12) (By similarity).
CC -!- SUBUNIT: Saposin B is a homodimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Lysosomal (By similarity).
CC -!- PTM: This precursor is proteolytically processed to 4 small
CC peptides, which are similar to each other and are sphingolipid
CC hydrolase activator proteins (By similarity).
CC -!- SIMILARITY: Contains 2 saposin A-type domains.
CC -!- SIMILARITY: Contains 4 saposin B-type domains.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; AF003471; BAA19914.1; -; mRNA.
DR EMBL; AF108656; AAF05899.1; -; mRNA.
DR HSSP; Q92739; IN69.
DR Ensembl; ENSGALG0000004769; Gallus gallus.
DR InterPro; IPR009007; Rept_Aspartc_cat.
DR InterPro; IPR003119; Sapa.
DR InterPro; IPR007856; SapaB_1.
DR InterPro; IPR008138; SapaB_2.
DR InterPro; IPR008140; SapaB_sub.
DR InterPro; IPR008373; Saposin.
DR InterPro; IPR008139; SaposinB.
DR Pfam; PF02199; Sapa; 2.
DR Pfam; PF05184; SapaB_1; 4.
DR Pfam; PF03489; SapaB_2; 4.
DR PRINTS; PR01797; SAPOSIN.
DR ProDom; PD001732; SapaB_sub; 1.
DR SMART; SM00162; SAPA; 2.
DR SMART; SM00741; Sapa; 4.
DR PROSITE; PS1110; SAP A; 2.
DR PROSITE; PS50015; SAP B; 4.
DR Direct protein sequencing; Glycoprotein; GM2-gangliosidosis;
DR Lipid metabolism; Lysosome; Repeat; Signal; Sphingolipid metabolism.
FT SIGNAL 1 17 Potential.
FT PROPEP 18 60
FT CHAIN 61 143 Saposin A.
FT PROPEP 145 193
FT CHAIN 194 276 Saposin B.
FT PROPEP 278 305
FT CHAIN 307 387 Saposin C.
FT PROPEP 389 398
FT CHAIN 399 480 Saposin D.
FT PROPEP 482 518
FT DOMAIN 19 59 Saposin A-type 1.
FT DOMAIN 61 143 Saposin B-type 1.
FT DOMAIN 194 277 Saposin B-type 2.
FT DOMAIN 307 388 Saposin B-type 3.
FT DOMAIN 399 480 Saposin B-type 4.
FT DOMAIN 482 518 Saposin A-type 2.

FT CARBOHYD	81	N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD	214	N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD	328	N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD	420	N-linked (GlcNAc. . .) (Potential).
FT DISULFID	64	By similarity.
FT DISULFID	67	By similarity.
FT DISULFID	95	By similarity.
FT DISULFID	197	By similarity.
FT DISULFID	200	By similarity.
FT DISULFID	229	By similarity.
FT DISULFID	311	By similarity.
FT DISULFID	314	By similarity.
FT DISULFID	342	By similarity.
FT DISULFID	406	By similarity.
FT DISULFID	434	By similarity.
FT CONFLICT	94	R -> T (in Ref. 2).
FT CONFLICT	486	E -> D (in Ref. 2).
SQ SEQUENCE	518 AA; 57601 MW; B803000E991C3963 CRC64;	

Query Match	60.2%;	Score 1679.5;	DB 1;	Length 518;
Best Local Similarity	57.4%;	Pred. No. 3.1e-101;		
Matches 301;	Conservative 96;	Mismatches 114;	Indels 13;	Gaps 5;

Qy	4	LFLASLIGALAGPVLGLKECTRGSAVWCQNVKATSCGAVKHCLQTVWKNKPTVKSLPC	63
Db	5	LLTLGLLAANAVASPVLMQKCAKGPVWCOSLRASOCGAVKHCCQNVWSPKPAVNSIPC	64
Qy	64	DICKVVTAAGDMLKDNATEEEILVLEKTCDWLPKPNMSASCKEIVDSYLPVLDIING	123
Db	65	DLCKELTVVGVKLVKNGTEDEIRSYLEKRCFELPDQGLASECKEIVDSYLPVINDMIKE	124
Qy	124	EMSPRGVCSALNICESLKHLELNHQQQLSKNIPBLDMTEVVAVPMANIPLLLYPOD	183
Db	125	EPDKPEVVCSSALSCLSQSLKHLAAMKQLQSNKIPELDFSELTSPFMANVPLLLYPQD	184
Qy	184	GPRSKPQPKNGDVCQDCIQMWTDIQTAVRTNSTFVQALVHVKEECDRLGPGMADICKN	243
Db	185	KPKQK--SKATEDVQCDCIRLVTVQEAVRTNATFVKSVAHAKEECDRLGPGMSDMCKS	242
Qy	244	YISQYSEIAIQMMHM---QPKICALVGFQDEVKEMPMQTLVPAKASKNVIPALELVE	300
Db	243	YISEYSLAIQMMHMKDQKPKICAMVGFQCSVKSVPQLTLVPAQVHVE-----VKWE	296
Qy	301	PIKHEVPAKSDVYCEVCEFLVKEVTKLIDNNKTEKEILDAPDKMCKSLPKSLSEECQEV	360
Db	297	TVEKATVQEKTFVSVCIECTMWKEVTGLLESNKTEEEIVHEMEVVCYLLPASVKDQCKDF	356
Qy	361	VDYGSISLTLLEVSPELVCSMLHLCSTGLPALTVHTVTPKDGCGFCECKLVGYLD	420
Db	357	IEVYQALIDMLLEATNPVAVCVMLKCAANKPQQPV--VKPA--GGFCDCIKRMIVAYAD	414
Qy	421	RNLEKNTKQEIILAALEKGCFLPDYQKQCDQFVAEYEPVLIEILVEVMDPSFVCLKIG	480
Db	415	KELEKNATTTEIEALLEKVCHEFLPESVDCQVQVEQVEPVVQVLLAEMMDPTFVCTKLG	474
Qy	481	ACPSAHKPLLGTEKCIWPGSYWCNTETAACNAVEHCKRHVN	524
Db	475	VCGAACKPLLGEDACVWNGPGYWCNKMETAACNAVDHCRHVN	518

Search completed: January 13, 2006, 16:34:21
Job time : 202.536 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 13, 2006, 16:26:00 ; Search time 54.6556 Seconds
(without alignments)
792.637 Million cell updates/sec

Title: US-10-801-517-1
Perfect score: 2789
Sequence: 1 MYALFLASLILGALAGPVL.....NTETAAQNAVEHCKRHVWN 524

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5 COMB.pdp:*
2: /cgn2_6/ptodata/1/iaa/6 COMB.pdp:*
3: /cgn2_6/ptodata/1/iaa/H COMB.pdp:*
4: /cgn2_6/ptodata/1/iaa/PCTRUS COMB.pdp:*
5: /cgn2_6/ptodata/1/iaa/RE COMB.pdp:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pdp:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2789	100.0	524	2	US-09-352-548-1
2	2789	100.0	524	2	US-09-949-016-6272
3	2789	100.0	524	2	US-08-928-074-23
4	2789	100.0	535	2	US-09-949-016-8603
5	2766.5	99.2	523	1	US-08-100-247-2
6	2766.5	99.2	523	2	US-08-756-031-2
7	2759.5	98.9	523	1	US-08-232-513A-3
8	2757.5	98.9	523	1	US-08-483-146A-2
9	2757.5	98.9	523	1	US-08-484-594A-2
10	2757.5	98.9	523	2	US-09-076-258A-2
11	431	15.5	81	2	US-09-352-548-2
12	418.5	15.0	80	1	US-08-584-671-15
13	418.5	15.0	80	2	US-09-027-376-15
14	415.5	14.9	80	2	US-09-094-192-15
15	412	14.8	80	1	US-08-100-247-3
16	412	14.8	80	1	US-08-483-146A-3
17	412	14.8	80	1	US-08-232-513A-4
18	412	14.8	80	1	US-08-484-594A-3
19	412	14.8	80	2	US-09-076-258A-3
20	412	14.8	80	2	US-08-756-031-3
21	412	14.8	80	2	US-08-928-074-24
22	350.5	12.6	381	1	US-09-193-877-2
23	349.5	12.5	381	1	US-09-949-016-10057
24	327	11.7	61	1	US-08-584-671-13
25	327	11.7	61	2	US-09-027-376-13
26	327	11.7	61	2	US-09-094-192-13
27	327	11.7	69	2	US-09-268-070-2

28	322	11.5	79	1	US-08-584-671-16	Sequence 16, Appl
29	322	11.5	79	2	US-09-027-376-16	Sequence 16, Appl
30	322	11.5	79	2	US-09-094-192-16	Sequence 16, Appl
31	321	11.5	79	1	US-08-584-671-14	Sequence 14, Appl
32	321	11.5	79	2	US-09-027-376-14	Sequence 14, Appl
33	321	11.5	79	2	US-09-094-192-14	Sequence 14, Appl
34	268.5	9.6	257	2	US-08-596-684F-7	Sequence 7, Appl
35	239.5	8.6	60	1	US-08-584-671-12	Sequence 12, Appl
36	239.5	8.6	60	2	US-09-027-376-12	Sequence 12, Appl
37	239.5	8.6	60	2	US-09-268-070-4	Sequence 4, Appl
38	239.5	8.6	60	2	US-09-094-192-12	Sequence 12, Appl
39	238.5	8.6	68	2	US-09-268-070-1	Sequence 1, Appl
40	211	7.6	40	2	US-09-780-438C-1	Sequence 1, Appl
41	208	7.5	67	2	US-09-268-070-3	Sequence 3, Appl
42	201	7.2	38	2	US-09-780-438C-2	Sequence 2, Appl
43	168.5	6.0	181	2	US-08-848-580-12	Sequence 12, Appl
44	168.5	6.0	181	2	US-08-488-123-12	Sequence 12, Appl
45	163	5.8	514	2	US-10-339-351-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1
US-09-352-548-1
; Sequence 1, Application US/09352548
; Patent No. 6500431
; GENERAL INFORMATION:
; APPLICANT: Gill, Parkash S.
; APPLICANT: Parkash S. Gill, M.D., Inc.
; TITLE OF INVENTION: No. 6500431el Inhibitors of Angiogenesis and Tumor Growth
; FILE REFERENCE: 017986-000410US
; CURRENT APPLICATION NUMBER: US/09/352,548
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: US 60/092,647
; EARLIER FILING DATE: 1998-07-13
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 524
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: prosaposin
; NAME/KEY: PEPTIDE
; LOCATION: (195)..(275)
; OTHER INFORMATION: Saposin B
US-09-352-548-1

Query Match	100.0%	Score 2789;	DB 2;	Length 524;
Best Local Similarity	100.0%;	Pred. No. 9.8e-243;	Mismatches 0;	Indels 0;
Matches 524;	Conservative 0;			Gaps 0;
Qy	1	MYALFLASLILGALAGPVLGLKCEKTRGSVAVCQNVKTASDCGAVKHCLQTVWVKPTVKS	60	
Db	1	MYALFLASLILGALAGPVLGLKCEKTRGSVAVCQNVKTASDCGAVKHCLQTVWVKPTVKS	60	
Qy	61	LPDCIKDVVTAAGMDMLKONATEEILVLYLEKCDMLPKPNMSASCKEIVDSYLPVLIDI	120	
Db	61	LPDCIKDVVTAAGMDMLKONATEEILVLYLEKCDMLPKPNMSASCKEIVDSYLPVLIDI	120	
Qy	121	IKGEMSRPGVCALNLCESLQHLAELNHOKLESNKIPELDMTEVVAFPFMANIPULLY	180	
Db	121	IKGEMSRPGVCALNLCESLQHLAELNHOKLESNKIPELDMTEVVAFPFMANIPULLY	180	
Qy	181	PQDGRSKPQPKNGDVQCDCIQMVTIDIQTAVRTNSTFVQALVEHVKECDRLGPGMADI	240	
Db	181	PQDGRSKPQPKNGDVQCDCIQMVTIDIQTAVRTNSTFVQALVEHVKECDRLGPGMADI	240	
Qy	241	CKNYISQYSBIAIQMMHMQPKBIKALVGFCDVEKMPMTLVPKAVSKNVI PALELVE	300	
Db	241	CKNYISQYSBIAIQMMHMQPKBIKALVGFCDVEKMPMTLVPKAVSKNVI PALELVE	300	

QY 301 PIKGEVPAKSDVYCEVCEFLVKEVTKLIDNNKTEKEILDADFKMCKSLPKSLSECEQEV 360
DB 301 PIKGEVPAKSDVYCEVCEFLVKEVTKLIDNNKTEKEILDADFKMCKSLPKSLSECEQEV 360
QY 361 VDTYSSILSILLREVSPELVCSMLHLCGSTRLPALTTHVTQPKDGGCFCEVCKKLVGYLD 420
DB 361 VDTYSSILSILLREVSPELVCSMLHLCGSTRLPALTTHVTQPKDGGCFCEVCKKLVGYLD 420
QY 421 RNLEKNSTKQBIILAALRGCSFLPDYQKQCDQFVAEYEPVLIELVEMDPSFVCLKIG 480
DB 421 RNLEKNSTKQBIILAALRGCSFLPDYQKQCDQFVAEYEPVLIELVEMDPSFVCLKIG 480
QY 481 APCSAHKPLLGTEKCIWGPSYWCQNTETAACNAVEHCKRHVN 524
DB 481 APCSAHKPLLGTEKCIWGPSYWCQNTETAACNAVEHCKRHVN 524
RESULT 2
US-09-949-016-6272
; Sequence 6272, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6272
; LENGTH: 524
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6272
Query Match 100.0%; Score 2789; DB 2; Length 524;
Best Local Similarity 100.0%; Pred. No. 9.8e-243;
Matches 524; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MYALFLASLLGAALAGPVLGKECTRGSAVWCQNVKTASDCGAVKHCLQTVWNKPTVKS 60
DB 1 MYALFLASLLGAALAGPVLGKECTRGSAVWCQNVKTASDCGAVKHCLQTVWNKPTVKS 60
QY 61 LPCDICKDVVTAAGDMLKDNATEBEILVYLEKTCDWLPKPNMSASCKEIVDSYLPVLDI 120
DB 61 LPCDICKDVVTAAGDMLKDNATEBEILVYLEKTCDWLPKPNMSASCKEIVDSYLPVLDI 120
QY 121 IKGMSRPGEVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVWAPFMANIPLLLY 180
DB 121 IKGMSRPGEVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVWAPFMANIPLLLY 180
QY 181 PQDGRSPKQPKDNGDVCDICIQMTVDIQTAVRTNSTFVQALVEHVKEBCECDRLGPGMADI 240
DB 181 PQDGRSPKQPKDNGDVCDICIQMTVDIQTAVRTNSTFVQALVEHVKEBCECDRLGPGMADI 240
QY 241 CKNYISQYSEIAIQMMHMQPKIEICALVGFCDVEKMPQTLVPAKVASKNVIPALELVE 300
DB 241 CKNYISQYSEIAIQMMHMQPKIEICALVGFCDVEKMPQTLVPAKVASKNVIPALELVE 300
QY 301 PIKGEVPAKSDVYCEVCEFLVKEVTKLIDNNKTEKEILDADFKMCKSLPKSLSECEQEV 360
DB 301 PIKGEVPAKSDVYCEVCEFLVKEVTKLIDNNKTEKEILDADFKMCKSLPKSLSECEQEV 360
QY 361 VDTYSSILSILLREVSPELVCSMLHLCGSTRLPALTTHVTQPKDGGCFCEVCKKLVGYLD 420

DB 361 VDTYSSILSILLREVSPELVCSMLHLCGSTRLPALTTHVTQPKDGGCFCEVCKKLVGYLD 420
QY 421 RNLEKNSTKQBIILAALRGCSFLPDYQKQCDQFVAEYEPVLIELVEMDPSFVCLKIG 480
DB 421 RNLEKNSTKQBIILAALRGCSFLPDYQKQCDQFVAEYEPVLIELVEMDPSFVCLKIG 480
QY 481 APCSAHKPLLGTEKCIWGPSYWCQNTETAACNAVEHCKRHVN 524
DB 481 APCSAHKPLLGTEKCIWGPSYWCQNTETAACNAVEHCKRHVN 524
RESULT 3
US-08-928-074-23
; Sequence 23, Application US/08928074
; Patent No. 6849602
; GENERAL INFORMATION:
; APPLICANT: O'Brien, John S.
; TITLE OF INVENTION: METHODS FOR ALLEVIATING NEUROPATHIC PAIN
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA: US/08/928,074
; APPLICATION NUMBER: 08/611,307
; FILING DATE: 11-SEP-1997
; PRIOR APPLICATION NUMBER: 08/611,307
; FILING DATE: 05-MAR-1996
; PRIOR APPLICATION DATA: PCT/US97/04143
; APPLICATION NUMBER: 05-MAR-1996
; FILING DATE: 05-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Ph.D., Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07256/024001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 524 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-928-074-23
Query Match 100.0%; Score 2789; DB 2; Length 524;
Best Local Similarity 100.0%; Pred. No. 9.8e-243;
Matches 524; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MYALFLASLLGAALAGPVLGKECTRGSAVWCQNVKTASDCGAVKHCLQTVWNKPTVKS 60
DB 1 MYALFLASLLGAALAGPVLGKECTRGSAVWCQNVKTASDCGAVKHCLQTVWNKPTVKS 60
QY 61 LPCDICKDVVTAAGDMLKDNATEBEILVYLEKTCDWLPKPNMSASCKEIVDSYLPVLDI 120
DB 61 LPCDICKDVVTAAGDMLKDNATEBEILVYLEKTCDWLPKPNMSASCKEIVDSYLPVLDI 120
QY 121 IKGMSRPGEVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVWAPFMANIPLLLY 180
DB 121 IKGMSRPGEVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVWAPFMANIPLLLY 180
QY 181 PQDGRSPKQPKDNGDVCDICIQMTVDIQTAVRTNSTFVQALVEHVKEBCECDRLGPGMADI 240

Db 181 PDKGPRKPKQKNGDVCQDCIQVTDIQAVRTNSTFVQALVEHVKKECDRLGPGNADI 240
Qy 241 CKNYISQYSEIATQMMHMQPKKEICALVGFCDVCKMPQTLVPAKVASKNVIIPALELVE 300
Db 241 CKNYISQYSEIATQMMHMQPKKEICALVGFCDVCKMPQTLVPAKVASKNVIIPALELVE 300
Qy 301 PIKKEHVPAKSDYVCEVCEFLVKEVTKLIDNNKTEKEIILDADFKMCSKLPKSLSEBCEV 360
Db 301 PIKKEHVPAKSDYVCEVCEFLVKEVTKLIDNNKTEKEIILDADFKMCSKLPKSLSEBCEV 360
Qy 361 VDTYGSIIILSEVSPVLCVSMHLCSGTRLPALTTHVHTQPKDGGFCEVCKLVGYLD 420
Db 361 VDTYGSIIILSEVSPVLCVSMHLCSGTRLPALTTHVHTQPKDGGFCEVCKLVGYLD 420
Qy 421 RNLEKNSTQKIEILAALEKGSFLPDPYQKQCDQFVAEYEPVLEIILVEVMDPSFVCLKIG 480
Db 421 RNLEKNSTQKIEILAALEKGSFLPDPYQKQCDQFVAEYEPVLEIILVEVMDPSFVCLKIG 480
Qy 481 ACPSAHKPLLGTEKCIWGPSYWCNTTETAACQNAVEHCKRHVWN 524
Db 481 ACPSAHKPLLGTEKCIWGPSYWCNTTETAACQNAVEHCKRHVWN 524

RESULT 4

US-09-949-016-8603
; Sequence 8603, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8603
; LENGTH: 535
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8603

Query Match 100.0%; Score 2789; DB 2; Length 535;
Best Local Similarity 100.0%; Pred. No. 1e-242;
Matches 524; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MYALFLLASLLGALAGPVLGLKECTGSAVWQNVKTSADCGAVKHCLQTVWVKPTVKS 60
Db 12 MYALFLLASLLGALAGPVLGLKECTGSAVWQNVKTSADCGAVKHCLQTVWVKPTVKS 71
Qy 61 LPCDICKDVVTAAGDMLKDNATEBEEILVYLEKTCMDLPKPNMGSASCKEIVDSYLPVILDI 120
Db 72 LPCDICKDVVTAAGDMLKDNATEBEEILVYLEKTCMDLPKPNMGSASCKEIVDSYLPVILDI 131
Qy 121 IKGMSRPGVCSALNICSILQKHLAELNHQKLESNKIPELDMTEVVAPPMANIPILLY 180
Db 132 IKGMSRPGVCSALNICSILQKHLAELNHQKLESNKIPELDMTEVVAPPMANIPILLY 191
Qy 181 PQDGRPKPKQKNGDVCQDCIQVTDIQAVRTNSTFVQALVEHVKKECDRLGPGNADI 240
Db 192 PQDGRPKPKQKNGDVCQDCIQVTDIQAVRTNSTFVQALVEHVKKECDRLGPGNADI 251
Qy 241 CKNYISQYSEIATQMMHMQPKKEICALVGFCDVCKMPQTLVPAKVASKNVIIPALELVE 300
Db 252 CKNYISQYSEIATQMMHMQPKKEICALVGFCDVCKMPQTLVPAKVASKNVIIPALELVE 311

Qy 301 PIKKEHVPAKSDYVCEVCEFLVKEVTKLIDNNKTEKEIILDADFKMCSKLPKSLSEBCEV 360
Db 312 PIKKEHVPAKSDYVCEVCEFLVKEVTKLIDNNKTEKEIILDADFKMCSKLPKSLSEBCEV 371
Qy 361 VDTYGSIIILSEVSPVLCVSMHLCSGTRLPALTTHVHTQPKDGGFCEVCKLVGYLD 420
Db 372 VDTYGSIIILSEVSPVLCVSMHLCSGTRLPALTTHVHTQPKDGGFCEVCKLVGYLD 431
Qy 421 RNLEKNSTQKIEILAALEKGSFLPDPYQKQCDQFVAEYEPVLEIILVEVMDPSFVCLKIG 480
Db 432 RNLEKNSTQKIEILAALEKGSFLPDPYQKQCDQFVAEYEPVLEIILVEVMDPSFVCLKIG 491
Qy 481 ACPSAHKPLLGTEKCIWGPSYWCNTTETAACQNAVEHCKRHVWN 524
Db 492 ACPSAHKPLLGTEKCIWGPSYWCNTTETAACQNAVEHCKRHVWN 535

RESULT 5

US-08-100-247-2
; Sequence 2, Application US/08100247
; Patent No. 5571787
; GENERAL INFORMATION:
; APPLICANT: O'BRIEN, JOHN S.
; APPLICANT: KISHIMOTO, YASUO
; TITLE OF INVENTION: PROSAPOSIN AS A NEUROTROPHIC FACTOR
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: KNOBBE, MARTENS, OLSON AND BEAR
; STREET: 620 NEWPORT CENTER DRIVE SIXTEENTH FLOOR
; CITY: NEWPORT BEACH
; STATE: CA
; COUNTRY: USA
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/100,247
; FILING DATE: 19930730
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Israelsen, Ned A.
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: O'Brien.002A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-235-8550
; TELEFAX: 619-235-0176
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 523 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; IMMEDIATE SOURCE:
; CLONE: PROSAPOSIN
US-08-100-247-2

Query Match 99.2%; Score 2766.5; DB 1; Length 523;
Best Local Similarity 99.4%; Pred. No. 1e-240;
Matches 521; Conservative 2; Mismatches 0; Indels 1; Gaps 1;
Qy 1 MYALFLLASLLGALAGPVLGLKECTGSAVWQNVKTSADCGAVKHCLQTVWVKPTVKS 60
Db 1 MYALFLLASLLGALAGPVLGLKECTGSAVWQNVKTSADCGAVKHCLQTVWVKPTVKS 60
Qy 61 LPCDICKDVVTAAGDMLKDNATEBEEILVYLEKTCMDLPKPNMGSASCKEIVDSYLPVILDI 120

us-10-801-517-1.ra1

Db	61	LPDCIDKDVWTAAGDMLKDNATBEIILVLEKTCMDLPKPNMSASCKEIVDSYLPVILDI	120
Qy	121	IKGMSRPGVCVSALNLCESLOKHLAELNHQKLESNKIPELDMTEVWAPFMANIPLLIY	180
Db	121	IKGMSRPGVCVSALNLCESLOKHLAELNHQKLESNKIPELDMTEVWAPFMANIPLLIY	180
Qy	181	PODGPRSPQPKNDGNCVQDCIQMWTDIQTAVRTNSTFVQALVEHVKEECDRLPGCMADI	240
Db	181	PODGPRSPQPKD-GDVCQDCIQMWTDIQTAVRTNSTFVQALVEHVKEECDRLPGCMADI	239
Qy	241	CKNYISQYSEIATQMMHMQPKBEICALVGFCDVEKEMPQTLVPAKVASKNVIIPALIEYE	300
Db	240	CKNYISQYSEIATQMMHMQPKBEICALVGFCDVEKEMPQTLVPAKVASKNVIIPALDIYD	299
Qy	301	PIKCHEVPAKSDVYCEVCEFLVKEVTKLIDNNKTEKELIDAFKQWCSKLPKSLSEECQBV	360
Db	300	PIKCHEVPAKSDVYCEVCEFLVKEVTKLIDNNKTEKELIDAFKQWCSKLPKSLSEECQBV	359
Qy	361	VDITYGSSILSILLEEVSPELVCSMLHLCSGTRLPALTVMHTQPKDGGFCBVCKKLVGYLD	420
Db	360	VDITYGSSILSILLEEVSPELVCSMLHLCSGTRLPALTVMHTQPKDGGFCBVCKKLVGYLD	419
Qy	421	RNLEKNSTKQEILAALEKGCSPFPDPYQKQCDQFVAEYEPVILIEILVEWMDPSFVCLKIG	480
Db	420	RNLEKNSTKQEILAALEKGCSPFPDPYQKQCDQFVAEYEPVILIEILVEWMDPSFVCLKIG	479
Qy	481	ACPSAHKPLLLGTEKCIWGPSYWCQNTETAAOCNAVEHCKRHVWN	524
Db	480	ACPSAHKPLLGTEKCIWGPSYWCQNTETAAOCNAVEHCKRHVWN	523

RESULT 6
 US-08-756-031-2
 ; Sequence 2, Application US/08756031
 ; Patent No. 6590074
 ; GENERAL INFORMATION:
 ; APPLICANT: O'BRIEN, JOHN S.
 ; APPLICANT: KISHIMOTO, YASUO
 ; TITLE OF INVENTION: PROSAPOSIN AS A NEUROTROPHIC FACTOR
 ; NUMBER OF SEQUENCES: 5
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: KNOBBE, MARTENS, OLSON AND BEAR
 ; STREET: 620 NEWPORT CENTER DRIVE SIXTEENTH FLOOR
 ; CITY: NEWPORT BEACH
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 92660
 ; COMPUTER READABLE FORM: disk
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/756,031
 ; FILING DATE: 26-NOV-1996
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/100,247
 ; FILING DATE: 30-JUL-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Israelsen, Ned A.
 ; REGISTRATION NUMBER: 29,655
 ; REFERENCE/DOCKET NUMBER: O'BRIEN .002A
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 619-235-8550
 ; TELEFAX: 619-235-0176
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 523 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/100,247
; FILING DATE: 30-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UD 1643
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 523 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..523
; OTHER INFORMATION: /label= Hum_prosaposin
;
US-08-232-513A-3

Query Match 98.9%; Score 2759.5; DB 1; Length 523;
Best Local Similarity 99.2%; Pred. No. 4.5e-240;
Matches 520; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 1 MYALFLASLGAALAGPVGLKECTRGSAVWQNVKTASDCGAVKHCLQTVWVKPTVKS 60
DB 1 MYALFLASLGAALAGPVGLKECTRGSAVWQNVKTASDCGAVKHCLQTVWVKPTVKS 60
QY 61 LPCDICKDVVTAAGDMLKONATEEEILVLEKTCDWLPKPNMSASCKEIVDSYLPVLDI 120
DB 61 LPCDICKDVVTAAGDMLKONATEEEILVLEKTCDWLPKPNMSASCKEIVDSYLPVLDI 120
QY 121 IKGEMSRPGVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVAVPFMANIPALLY 180
DB 121 IKGEMSRPGVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVAVPFMANIPALLY 180
QY 181 PDGPRSKPQPKD-GDVQCDCIQMVTDIQTAVRTNSTFVQALVEHVKEBCDRLGPGWADI 240
DB 181 PDGPRSKPQPKD-GDVQCDCIQMVTDIQTAVRTNSTFVQALVEHVKEBCDRLGPGWADI 239
QY 241 CKNYISQYSEIAIQMMHMQPKKEICALVGFCDEVKEMPMQTLVPAKVASKNVI PALELVE 300
DB 240 CKNYISQYSEIAIQMMHMQPKKEICALVGFCDEVKEMPMQTLVPAKVASKNVI PALELVE 299
QY 301 PIKKEHVPAKSDVYCEVCEFLVKEVTKLIDNNKTEKEILDAFDKMCCKLPKSLSEBCQEV 360
DB 300 PIKKEHVPAKSDVYCEVCEFLVKEVTKLIDNNKTEKEILDAFDKMCCKLPKSLSEBCQEV 359
QY 361 VDTYGSLSILLEEVSPELVCSMLHLCSTRLPALTVHVTPQKDGFCFCEVCKKLVGYLD 420
DB 360 VDTYGSLSILLEEVSPELVCSMLHLCSTRLPALTVHVTPQKDGFCFCEVCKKLVGYLD 419
QY 421 RNLEKNSKQEIILAALEKGCFLPDPYQKQCDQFVAEYEPVLIEILVEVMDPSFVCLKIG 480
DB 420 RNLEKNSKQEIILAALEKGCFLPDPYQKQCDQFVAEYEPVLIEILVEVMDPSFVCLKIG 479
QY 481 ACPSAHKPLLGTEKCIWGPSYWCNTETAACQNAVECHKRHVN 524
DB 480 ACPSAHKPLLGTEKCIWGPSYWCNTETAACQNAVECHKRHVN 523

RESULT 8
US-08-483-146A-2
; Sequence 2, Application US/08483146A
; Patent No. 5696080
; GENERAL INFORMATION:
; APPLICANT: O'Brien, John S.
; APPLICANT: Kishimoto, Yasuo
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS
; TITLE OF INVENTION: COMPRISING PROSAPOSIN AND NEUROTROPHIC PEPTIDES DERIVED THEREFROM

```

```

; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson and Bear
; STREET: 620 Newport Center Blvd. 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,146A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Israel, Ned A.
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: MYELOS.002DVI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-235-8550
; TELEFAX: 619-235-0176
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 523 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: N-terminal
;
US-08-483-146A-2

Query Match 98.9%; Score 2757.5; DB 1; Length 523;
Best Local Similarity 99.2%; Pred. No. 6.7e-240;
Matches 520; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 1 MYALFLASLGAALAGPVGLKECTRGSAVWQNVKTASDCGAVKHCLQTVWVKPTVKS 60
DB 1 MYALFLASLGAALAGPVGLKECTRGSAVWQNVKTASDCGAVKHCLQTVWVKPTVKS 60
QY 61 LPCDICKDVVTAAGDMLKONATEEEILVLEKTCDWLPKPNMSASCKEIVDSYLPVLDI 120
DB 61 LPCDICKDVVTAAGDMLKONATEEEILVLEKTCDWLPKPNMSASCKEIVDSYLPVLDI 120
QY 121 IKGEMSRPGVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVAVPFMANIPALLY 180
DB 121 IKGEMSRPGVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVAVPFMANIPALLY 180
QY 181 PDGPRSKPQPKD-GDVQCDCIQMVTDIQTAVRTNSTFVQALVEHVKEBCDRLGPGWADI 240
DB 181 PDGPRSKPQPKD-GDVQCDCIQMVTDIQTAVRTNSTFVQALVEHVKEBCDRLGPGWADI 239
QY 241 CKNYISQYSEIAIQMMHMQPKKEICALVGFCDEVKEMPMQTLVPAKVASKNVI PALELVE 300
DB 240 CKNYISQYSEIAIQMMHMQPKKEICALVGFCDEVKEMPMQTLVPAKVASKNVI PALELVE 299
QY 301 PIKKEHVPAKSDVYCEVCEFLVKEVTKLIDNNKTEKEILDAFDKMCCKLPKSLSEBCQEV 360
DB 300 PIKKEHVPAKSDVYCEVCEFLVKEVTKLIDNNKTEKEILDAFDKMCCKLPKSLSEBCQEV 359
QY 361 VDTYGSLSILLEEVSPELVCSMLHLCSTRLPALTVHVTPQKDGFCFCEVCKKLVGYLD 420
DB 360 VDTYGSLSILLEEVSPELVCSMLHLCSTRLPALTVHVTPQKDGFCFCEVCKKLVGYLD 419
QY 421 RNLEKNSKQEIILAALEKGCFLPDPYQKQCDQFVAEYEPVLIEILVEVMDPSFVCLKIG 480
DB 420 RNLEKNSKQEIILAALEKGCFLPDPYQKQCDQFVAEYEPVLIEILVEVMDPSFVCLKIG 479

```


Query Match 98.9%; Score 2757.5; DB 2; Length 523;
Best Local Similarity 99.2%; Pred. No. 6.7e-240;
Matches 520; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

Qy 1 MYALFLASLLGALAGPVLGLKECTRGSAVQCNVKTASDCGAVKHCLQTVWVKPTVKS 60
Db 1 MYALFLASLLGALAGPVLGLKECTRGSAVQCNVKTASDCGAVKHCLQTVWVKPTVKS 60

Qy 61 LPCDICKOVVTAAGDMLKONATEEILVYLEKTCMDLPKNMSASCKEIVDSYLPVLDI 120
Db 61 LPCDICKOVVTAAGDMLKONATEEILVYLEKTCMDLPKNMSASCKEIVDSYLPVLDI 120

Qy 121 IKGEMSRPGVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVAPFMANIPLLLY 180
Db 121 IKGEMSRPGVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVAPFMANIPLLLY 180

Qy 181 PQDGRSKPQKONGVQDCIQMWTDIQTAVRTNSTFVQALVEHVKEBCDRLGPGMADI 240
Db 181 PQDGRSKPQKONGVQDCIQMWTDIQTAVRTNSTFVQALVEHVKEBCDRLGPGMADI 239

Qy 241 CKNYISQYSIAIQMMHMQPKKEICALVGFCDVEKMPQTLVPAKVASKNVIPALELVE 300
Db 240 CKNYISQYSIAIQMMHMQPKKEICALVGFCDVEKMPQTLVPAKVASKNVIPALDLVD 299

Qy 301 PIKKHEVPAKSDVYCEVCEFLVKEVTKLIDNNKTEKEILDAFDKMCCKLPSLSECOEV 360
Db 300 PIKKHEVPAKSDVYCEVCEFLVKEVTKLIDNNKTEKEILDAFDKMCCKLPSLSECOEV 359

Qy 361 VDTYGSILSILLEEVSPELVCSMLHLCSGTRLPALTVHVTQPKDGGFCVCKLVGYLD 420
Db 360 VDTYGSILSILLEEVSPELVCSMLHLCSGTRLPALTVHVTQPKDGGFCVCKLVGTLD 419

Qy 421 RNLEKSTKEIILAALEKGSFLPDPYKQCDQFVAEYEPVLIEILVEVMDPSFVCLKIG 480
Db 420 RNLEKSTKEIILAALEKGSFLPDPYKQCDQFVAEYEPVLIEILVEVMDPSFVCLKIG 479

Qy 481 ACPSAHKPLGTEKINGPSYWCQNTETAQCNVHECKRHVN 524
Db 480 ACPSAHKPLGTEKINGPSYWCQNTETAQCNVHECKRHVN 523

RESULT 11
US-09-352-548-2
; Sequence 2, Application US/09352548
; Patent No. 6500431
; GENERAL INFORMATION:
; APPLICANT: Gill, Parkash S.
; TITLE OF INVENTION: No. 6500431el Inhibitors of Angiogenesis and Tumor Growth
; FILE REFERENCE: 017986-000410US
; CURRENT APPLICATION NUMBER: US/09/352,548
; EARLIER FILING DATE: 1999-07-12
; EARLIER FILING DATE: 1998-07-13
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 2
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Saposin B
US-09-352-548-2

Query Match 15.5%; Score 431; DB 2; Length 81;
Best Local Similarity 100.0%; Pred. No. 2.3e-31;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 195 GDVQCDCIQMWTDIQTAVRTNSTFVQALVEHVKEBCDRLGPGMADICKNYISQYSIAIQ 254
Db 1 GDVQCDCIQMWTDIQTAVRTNSTFVQALVEHVKEBCDRLGPGMADICKNYISQYSIAIQ 60

Qy 255 MMHMQPKKEICALVGFCDVEK 275
Db 61 MMHMQPKKEICALVGFCDVEK 81

RESULT 12
US-08-584-671-15
; Sequence 15, Application US/08584671
; Patent No. 5910568
; GENERAL INFORMATION:
; APPLICANT: HAMBERSTEDT, ROY H, BARBATO, GUY F,
; APPLICANT: CRAMER, PALMER
; TITLE OF INVENTION: MOLECULE INVOLVED IN BINDING OF SPERM
; TITLE OF INVENTION: TO EGG SURFACES AND PROCEDURES FOR USE OF THIS MOLECULE
; TITLE OF INVENTION: TO ENHANCE OR DECREASE POTENTIAL FERTILITY
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INTELLECTUAL PROPERTY OFFICE, THE PENNSYLVANIA
; ADDRESSEE: STATE UNIVERSITY
; STREET: 113 TECHNOLOGY CENTER
; CITY: UNIVERSITY PARK
; STATE: PENNSYLVANIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 16802-7000
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: NEC 286
; OPERATING SYSTEM: DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,671
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MONAHAN, THOMAS J
; REGISTRATION NUMBER: 29835
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 814-865-6277
; TELEFAX: 814-865-3591
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 80
; TYPE: AMINO ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: UNKNOWN
US-08-584-671-15

Query Match 15.0%; Score 418.5; DB 1; Length 80;
Best Local Similarity 98.8%; Pred. No. 3.1e-30;
Matches 80; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 128 PGEVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVAPFMANIPLLLYPQDGP 187
Db 1 PGEVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVAPFMANIPLLLYPQDGP 59

Qy 188 KPQKONGDVQDCIQMWTDI 208
Db 60 KPQKONGDVQDCIQMWTDI 80

RESULT 13
US-09-027-376-15
; Sequence 15, Application US/09027376
; Patent No. 6004586
; GENERAL INFORMATION:
; APPLICANT: HAMBERSTEDT, ROY H, BARBATO, GUY F,
; APPLICANT: CRAMER, PALMER
; TITLE OF INVENTION: MOLECULE INVOLVED IN BINDING OF SPERM
; TITLE OF INVENTION: TO EGG SURFACES AND PROCEDURES FOR USE OF THIS MOLECULE
; TITLE OF INVENTION: TO ENHANCE OR DECREASE POTENTIAL FERTILITY
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:

ADDRESSEE: INTELLECTUAL PROPERTY OFFICE, THE PENNSYLVANIA
ADDRESSEE: STATE UNIVERSITY
STREET: 113 TECHNOLOGY CENTER
CITY: UNIVERSITY PARK
STATE: PENNSYLVANIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 16802-7000
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: NEC 286
OPERATING SYSTEM: DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/027,376
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/584,671
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: MONAHAN, THOMAS J
REGISTRATION NUMBER: 29835
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 814-865-6277
TELEFAX: 814-865-3591
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 80
TYPE: AMINO ACID
STRANDEDNESS: SINGLE
TOPOLOGY: UNKNOWN
US-09-027-376-15
Query Match 15.0%; Score 418.5; DB 2; Length 80;
Best Local Similarity 98.8%; Pred. No. 3.1e-30;
Matches 80; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
Qy 128 PGEVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVVAPFMANIPLLLYPQDGP 187
Db 1 PGEVC-ALNLCESLQKHLAELNHQKLESNKIPELDMTEVVAPFMANIPLLLYPQDGP 59
Qy 188 KPQKNGDVCDCIQMTDI 208
Db 60 KPQKNGDVCDCIQMTDI 80
RESULT 14
US-09-094-192-15
Sequence 15, Application US/09094192
Patent No. 6103483
GENERAL INFORMATION:
APPLICANT: HAMMERSTEDT, ROY H., BARBATO, GUY F.
APPLICANT: CRAMER, PALMER
TITLE OF INVENTION: MOLECULE INVOLVED IN BINDING OF SPERM TO EGG SURFACES AND PRO
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESSES:
ADDRESSEE: INTELLECTUAL PROPERTY OFFICE, THE PENNSYLVANIA STATE UNIVERSITY
STREET: 113 TECHNOLOGY CENTER
CITY: UNIVERSITY PARK
STATE: PENNSYLVANIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 16802-7000
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: NEC 286
OPERATING SYSTEM: DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/094,192
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:

NAME: MONAHAN, THOMAS J
REGISTRATION NUMBER: 29835
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 814-865-6277
TELEFAX: 814-865-3591
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 80
TYPE: AMINO ACID
STRANDEDNESS: SINGLE
TOPOLOGY: UNKNOWN
US-09-094-192-15
Query Match 14.9%; Score 415.5; DB 2; Length 80;
Best Local Similarity 97.5%; Pred. No. 5.7e-30;
Matches 79; Conservative 1; Mismatches 0; Indels 1; Gaps 1;
Qy 128 PGEVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVVAPFMANIPLLLYPQDGP 187
Db 1 PGEVC-ALNLCESLQKHLAELNHQKLESNKIPELDMTEVVAPFMANIPLLLYPQDGP 59
Qy 188 KPQKNGDVCDCIQMTDI 208
Db 60 KPQKNGDVCDCIQMTDI 80
RESULT 15
US-08-100-247-3
Sequence 3, Application US/08100247
Patent No. 5571787
GENERAL INFORMATION:
APPLICANT: O'BRIEN, JOHN S.
APPLICANT: KISHIMOTO, YASUO
TITLE OF INVENTION: PROSAPOSIN AS A NEUROTROPIC FACTOR
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESSES:
ADDRESSEE: KNOBBE, MARTENS, OLSON AND BEAR
STREET: 620 NEWPORT CENTER DRIVE SIXTEENTH FLOOR
CITY: NEWPORT BEACH
STATE: CA
COUNTRY: USA
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/100,247
FILING DATE: 19930730
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Israelsen, Ned A.
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: O'Brien.002A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-235-8550
TELEFAX: 619-235-0176
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 80 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
IMMEDIATE SOURCE:
CLONE: SAPOSIN C
US-08-100-247-3

Query Match 14.8%; Score 412; DB 1; Length 80;
Best Local Similarity 100.0%; Pred. No. 1.2e-29;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 311 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDAPDKMCKSLPKSLSEECQEVVDYTGSSILS 370
Db 1 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDAPDKMCKSLPKSLSEECQEVVDYTGSSILS 60
Qy 371 ILLEEVSPELVCSMLHLCSG 390
Db 61 ILLEEVSPELVCSMLHLCSG 80

Search completed: January 13, 2006, 16:36:34
Job time : 55.6556 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.1.6
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 13, 2006, 16:26:40 ; Search time 99.7682 Seconds
(without alignments)
2194.512 Million cell updates/sec

Title: US-10-801-517-1
Perfect score: 2789
Sequence: 1 MYALFLASLLGALAGPVL.....NTETAQCNVABCKRHVN 524

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues
Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pap:
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pap:
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pap:
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pap:
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pap:
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pap:

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	2789	100.0	524	3	US-09-870-759-60
2	2789	100.0	524	3	US-09-751-708A-60
3	2789	100.0	524	4	US-10-267-502-386
4	2789	100.0	524	4	US-10-408-765A-1207
5	2789	100.0	524	4	US-10-746-442-23
6	2789	100.0	524	4	US-10-428-817A-56
7	2789	100.0	524	5	US-10-801-517-1
8	2789	100.0	524	5	US-10-473-127-1865
9	2789	100.0	524	5	US-10-473-127-1866
10	2789	100.0	524	5	US-10-473-127-1868
11	2789	100.0	524	5	US-10-473-127-1869
12	2789	100.0	524	5	US-10-473-127-1871
13	2789	100.0	524	5	US-10-473-127-1873
14	2789	100.0	524	5	US-10-473-127-1878
15	2789	100.0	524	5	US-10-473-127-1879
16	2789	100.0	524	5	US-10-473-127-1880
17	2789	100.0	524	5	US-10-473-127-1881
18	2789	100.0	524	5	US-10-473-127-1882
19	2789	100.0	524	5	US-10-473-127-2041
20	2789	100.0	524	6	US-11-036-867-23
21	2779	99.6	524	5	US-10-473-127-1874
22	2777.5	99.6	527	3	US-09-870-759-61
23	2777.5	99.6	527	3	US-09-751-708A-61
24	2777.5	99.6	527	4	US-10-060-036-73
25	2777.5	99.6	527	4	US-10-428-817A-57
26	2777.5	99.6	527	5	US-10-473-127-1870
27	2777.5	99.6	527	5	US-10-473-127-1876

28	2772.5	99.4	523	5	US-10-473-127-1877	Sequence 1877, Ap
29	2768	99.2	526	5	US-10-473-127-1875	Sequence 1875, Ap
30	2767.5	99.2	527	5	US-10-473-127-1872	Sequence 1872, Ap
31	2757.5	98.9	523	3	US-09-767-007A-2	Sequence 2, Appl
32	2731	97.9	522	3	US-10-618-281-38	Sequence 38, Appl
33	2449.5	87.8	479	3	US-09-978-418-40	Sequence 40, Appl
34	2449.5	87.8	479	5	US-10-485-231-40	Sequence 40, Appl
35	1969	70.6	554	4	US-10-205-194-176	Sequence 176, App
36	1201	43.1	521	4	US-10-276-162-1	Sequence 1, Appl
37	1201	43.1	521	6	US-11-002-844-1	Sequence 1, Appl
38	1151.5	41.3	227	4	US-10-452-858C-11	Sequence 11, Appl
39	1139.5	40.9	531	3	US-09-833-245-903	Sequence 903, App
40	1125	40.3	210	5	US-10-473-127-1867	Sequence 1867, Ap
41	1093	39.2	209	4	US-10-043-487-340	Sequence 340, App
42	834.5	29.9	362	4	US-10-332-426-8	Sequence 8, Appl
43	552	19.8	953	4	US-10-267-502-385	Sequence 385, App
44	552	19.8	953	6	US-11-097-143-1959	Sequence 1959, Ap
45	545	19.5	241	4	US-10-108-260A-4529	Sequence 4529, Ap

RESULT 1
US-09-870-759-60
; Sequence 60, Application US/09870759
; Patent No. US20020177551A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 870759
; CURRENT APPLICATION NUMBER: US/09/870,759
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/208,128
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 60
; LENGTH: 524
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-870-759-60

Query Match 100.0%; Score 2789; DB 3; Length 524;
Best Local Similarity 100.0%; Pred. No. 1.6e-224;
Matches 524; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MYALFLASLLGALAGPVLGLKCECTRGSAVNCQNVKTASDCGAVKHCLQTWNKPTVKS	60
Db	1	MYALFLASLLGALAGPVLGLKCECTRGSAVNCQNVKTASDCGAVKHCLQTWNKPTVKS	60
QY	61	LPDCIDKDVVTAAGDMLKDNATEEEILVYLEKTCDWLPKPNMSASCKEIVDSVLPVLDI	120
Db	61	LPDCIDKDVVTAAGDMLKDNATEEEILVYLEKTCDWLPKPNMSASCKEIVDSVLPVLDI	120
QY	121	IKGMSRPEVCASALNLCESLOKHLAELNHQKLESNKIPELDMTEVAPFMANIPILLY	180
Db	121	IKGMSRPEVCASALNLCESLOKHLAELNHQKLESNKIPELDMTEVAPFMANIPILLY	180
QY	181	PQDGPSPQPKDNGDVQCDCIQMVTDIQTAVRTNSTFVQALVEHVKECDRLGPGMADI	240
Db	181	PQDGPSPQPKDNGDVQCDCIQMVTDIQTAVRTNSTFVQALVEHVKECDRLGPGMADI	240
QY	241	CKNYISQYSEIAIOMMMHQPKEICALVGFCDEKEMPMQTLVPAKVASKNVPALVELVE	300
Db	241	CKNYISQYSEIAIOMMMHQPKEICALVGFCDEKEMPMQTLVPAKVASKNVPALVELVE	300
QY	301	PIKKEHVPAKSDVYCVCEFLVKEVTKLIDNNKTEKILDAFDKMCCKLPKSLSECEQEV	360
Db	301	PIKKEHVPAKSDVYCVCEFLVKEVTKLIDNNKTEKILDAFDKMCCKLPKSLSECEQEV	360
QY	361	VDTYGSSILSLLEEVSPVLVCSMLHLCSTRLPALTVHTVTPQKDGFCVCKLVGYLD	420

ALIGNMENTS

Db 361 VDTYGSSTLSLLEEVSPVLCVSMHLCSTGLPALTVHVTQPKDGGFCEVCKLVGYLD 420
Qy 421 RNLEKNSKQBIILAEKGCSTFLPDYQKQCDQFVAEYEPVLIIEILVEVMDPSFVCLKIG 480
Db 421 RNLEKNSKQBIILAEKGCSTFLPDYQKQCDQFVAEYEPVLIIEILVEVMDPSFVCLKIG 480
Qy 481 ACPSAHKPLLTGTEKCIWGPSYWCNTETAACQNAVEHCKRHWN 524
Db 481 ACPSAHKPLLTGTEKCIWGPSYWCNTETAACQNAVEHCKRHWN 524

RESULT 2
US-09-751-708A-60
; Sequence 60, Application US/09751708A
; Publication No. US20030157113A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 751708
; CURRENT APPLICATION NUMBER: US/09/751,708A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/173,371
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 60
; LENGTH: 524
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-751-708A-60

Query Match 100.0%; Score 2789; DB 3; Length 524;
Best Local Similarity 100.0%; Pred. No. 1.6e-224;
Matches 524; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MYALFLLASLLGAALAGPVGLGKECTRGSAVWCQNVKTASDCGAVKHCLQTVWNNKPTVKS 60
Db 1 MYALFLLASLLGAALAGPVGLGKECTRGSAVWCQNVKTASDCGAVKHCLQTVWNNKPTVKS 60
Qy 61 LPDCICKDVVTAAGDMLKDNATEEILVLEKTCDWLPKPNMSASCKEIVDSYLPVLDI 120
Db 61 LPDCICKDVVTAAGDMLKDNATEEILVLEKTCDWLPKPNMSASCKEIVDSYLPVLDI 120
Qy 121 IKGMSRPGEVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVVAPFWMANIPLLLY 180
Db 121 IKGMSRPGEVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVVAPFWMANIPLLLY 180
Qy 181 PDGPRSKPQPKDNGDVQDCIQMVTDIQTAVRTNSTFVQALVEHVKECDRLGFGMADI 240
Db 181 PDGPRSKPQPKDNGDVQDCIQMVTDIQTAVRTNSTFVQALVEHVKECDRLGFGMADI 240
Qy 241 CKNYISOYSEIAIQMMHMQPKETCALVGFCDVEKEMPQTLVPAKASKNVI PALELVE 300
Db 241 CKNYISOYSEIAIQMMHMQPKETCALVGFCDVEKEMPQTLVPAKASKNVI PALELVE 300
Qy 301 PIKKEHVPKSDVYCEVCEFLVKEVTKLIDNNKTEKEILDADFKMCSKLPKSLSECCQEV 360
Db 301 PIKKEHVPKSDVYCEVCEFLVKEVTKLIDNNKTEKEILDADFKMCSKLPKSLSECCQEV 360
Qy 361 VDTYGSSTLSLLEEVSPVLCVSMHLCSTGLPALTVHVTQPKDGGFCEVCKLVGYLD 420
Db 361 VDTYGSSTLSLLEEVSPVLCVSMHLCSTGLPALTVHVTQPKDGGFCEVCKLVGYLD 420
Qy 421 RNLEKNSKQBIILAEKGCSTFLPDYQKQCDQFVAEYEPVLIIEILVEVMDPSFVCLKIG 480
Db 421 RNLEKNSKQBIILAEKGCSTFLPDYQKQCDQFVAEYEPVLIIEILVEVMDPSFVCLKIG 480
Qy 481 ACPSAHKPLLTGTEKCIWGPSYWCNTETAACQNAVEHCKRHWN 524
Db 481 ACPSAHKPLLTGTEKCIWGPSYWCNTETAACQNAVEHCKRHWN 524

RESULT 3

US-10-267-502-386
; Sequence 386, Application US/10267502
; Publication No. US20040071700A1
; GENERAL INFORMATION:
; APPLICANT: Kim, Jaeseob
; APPLICANT: Galant, Ron
; TITLE OF INVENTION: Obesity Linked Genes
; FILE REFERENCE: LSD-07416
; CURRENT APPLICATION NUMBER: US/10/267,502
; CURRENT FILING DATE: 2003-01-27
; NUMBER OF SEQ ID NOS: 439
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 386
; LENGTH: 524
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-267-502-386

Query Match 100.0%; Score 2789; DB 4; Length 524;
Best Local Similarity 100.0%; Pred. No. 1.6e-224;
Matches 524; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MYALFLLASLLGAALAGPVGLGKECTRGSAVWCQNVKTASDCGAVKHCLQTVWNNKPTVKS 60
Db 1 MYALFLLASLLGAALAGPVGLGKECTRGSAVWCQNVKTASDCGAVKHCLQTVWNNKPTVKS 60
Qy 61 LPDCICKDVVTAAGDMLKDNATEEILVLEKTCDWLPKPNMSASCKEIVDSYLPVLDI 120
Db 61 LPDCICKDVVTAAGDMLKDNATEEILVLEKTCDWLPKPNMSASCKEIVDSYLPVLDI 120
Qy 121 IKGMSRPGEVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVVAPFWMANIPLLLY 180
Db 121 IKGMSRPGEVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVVAPFWMANIPLLLY 180
Qy 181 PDGPRSKPQPKDNGDVQDCIQMVTDIQTAVRTNSTFVQALVEHVKECDRLGFGMADI 240
Db 181 PDGPRSKPQPKDNGDVQDCIQMVTDIQTAVRTNSTFVQALVEHVKECDRLGFGMADI 240
Qy 241 CKNYISOYSEIAIQMMHMQPKETCALVGFCDVEKEMPQTLVPAKASKNVI PALELVE 300
Db 241 CKNYISOYSEIAIQMMHMQPKETCALVGFCDVEKEMPQTLVPAKASKNVI PALELVE 300
Qy 301 PIKKEHVPKSDVYCEVCEFLVKEVTKLIDNNKTEKEILDADFKMCSKLPKSLSECCQEV 360
Db 301 PIKKEHVPKSDVYCEVCEFLVKEVTKLIDNNKTEKEILDADFKMCSKLPKSLSECCQEV 360
Qy 361 VDTYGSSTLSLLEEVSPVLCVSMHLCSTGLPALTVHVTQPKDGGFCEVCKLVGYLD 420
Db 361 VDTYGSSTLSLLEEVSPVLCVSMHLCSTGLPALTVHVTQPKDGGFCEVCKLVGYLD 420
Qy 421 RNLEKNSKQBIILAEKGCSTFLPDYQKQCDQFVAEYEPVLIIEILVEVMDPSFVCLKIG 480
Db 421 RNLEKNSKQBIILAEKGCSTFLPDYQKQCDQFVAEYEPVLIIEILVEVMDPSFVCLKIG 480
Qy 481 ACPSAHKPLLTGTEKCIWGPSYWCNTETAACQNAVEHCKRHWN 524
Db 481 ACPSAHKPLLTGTEKCIWGPSYWCNTETAACQNAVEHCKRHWN 524

RESULT 4
US-10-408-765A-1207
; Sequence 1207, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Faby, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME

```
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: PASTSEQ for Windows Version 4.0
; SEQ ID NO 1207
; LENGTH: 524
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-1207

Query Match      100.0%; Score 2789; DB 4; Length 524;
Best Local Similarity 100.0%; Pred. No. 1.6e-224;
Matches 524; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYALFLLASLLGAALAGPVLGLKECTRGSAVQNVKTASDCGAVKHCLQTVWVKPTVKS 60
DB 1 MYALFLLASLLGAALAGPVLGLKECTRGSAVQNVKTASDCGAVKHCLQTVWVKPTVKS 60

QY 61 LPDCICKDVVTAAGDMLKDNATEEELIVLEKTCDWLPKPNMSASCKEIVDSYLPVILDI 120
DB 61 LPDCICKDVVTAAGDMLKDNATEEELIVLEKTCDWLPKPNMSASCKEIVDSYLPVILDI 120

QY 121 IKGEMSRPGEVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVAPFMANIPLLY 180
DB 121 IKGEMSRPGEVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVAPFMANIPLLY 180

QY 181 PQDGPRSKPQPKDNGDVQCDCIQMVTDIQTAVRTNSTFVQALVEHVKEBCDRLGPGWADI 240
DB 181 PQDGPRSKPQPKDNGDVQCDCIQMVTDIQTAVRTNSTFVQALVEHVKEBCDRLGPGWADI 240

QY 241 CKNYISOYSEIAIQMMHMQPKKEICALVGFCDVEKEMPMQTLVPKAVASKNVIPAELVE 300
DB 241 CKNYISOYSEIAIQMMHMQPKKEICALVGFCDVEKEMPMQTLVPKAVASKNVIPAELVE 300

QY 301 PIKKEHVPAKSDYCEVCEFLVKEVTKLIDNNKTEKEIILDAPDKMCSKLPKSLSESCQEV 360
DB 301 PIKKEHVPAKSDYCEVCEFLVKEVTKLIDNNKTEKEIILDAPDKMCSKLPKSLSESCQEV 360

QY 361 VDTYGSIIILLEEVSPELVCSMLHLCSTRLPALTVHVTQPKDGFCEVCKLVGYLD 420
DB 361 VDTYGSIIILLEEVSPELVCSMLHLCSTRLPALTVHVTQPKDGFCEVCKLVGYLD 420

QY 421 RNLEKSTQKEILAALEKGCSEFLPDPYQKQCDQFVAEYEPVLIEILVEVMDPSFVCLKIG 480
DB 421 RNLEKSTQKEILAALEKGCSEFLPDPYQKQCDQFVAEYEPVLIEILVEVMDPSFVCLKIG 480

QY 481 ACPSAHKPLLGTEKCIWGPSYWCNTETAAQCNAVEHCKRHHVN 524
DB 481 ACPSAHKPLLGTEKCIWGPSYWCNTETAAQCNAVEHCKRHHVN 524

RESULT 5
US-10-746-442-23
; Sequence 23, Application US/10746442
; Publication No. US20040121958A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, John S.
; TITLE OF INVENTION: METHODS FOR ALLEVIATING NEUROPATHIC PAIN
; FILE REFERENCE: 07256/024001
; CURRENT APPLICATION NUMBER: US/10/746,442
; CURRENT FILING DATE: 2003-12-24
; PRIOR APPLICATION NUMBER: APPLICATION NUMBER: US/08/928,074
; PRIOR FILING DATE: FILING DATE: 1997-09-11
; PRIOR APPLICATION NUMBER: APPLICATION NUMBER: 08/611,307
; PRIOR FILING DATE: FILING DATE: 1996-03-05
; PRIOR APPLICATION NUMBER: APPLICATION NUMBER: PCT/US97/04143
; PRIOR FILING DATE: FILING DATE: 1996-03-05
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 23
; LENGTH: 524
; TYPE: PRT
```

```
; ORGANISM: Homo sapiens
US-10-746-442-23

Query Match      100.0%; Score 2789; DB 4; Length 524;
Best Local Similarity 100.0%; Pred. No. 1.6e-224;
Matches 524; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYALFLLASLLGAALAGPVLGLKECTRGSAVQNVKTASDCGAVKHCLQTVWVKPTVKS 60
DB 1 MYALFLLASLLGAALAGPVLGLKECTRGSAVQNVKTASDCGAVKHCLQTVWVKPTVKS 60

QY 61 LPDCICKDVVTAAGDMLKDNATEEELIVLEKTCDWLPKPNMSASCKEIVDSYLPVILDI 120
DB 61 LPDCICKDVVTAAGDMLKDNATEEELIVLEKTCDWLPKPNMSASCKEIVDSYLPVILDI 120

QY 121 IKGEMSRPGEVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVAPFMANIPLLY 180
DB 121 IKGEMSRPGEVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVAPFMANIPLLY 180

QY 181 PQDGPRSKPQPKDNGDVQCDCIQMVTDIQTAVRTNSTFVQALVEHVKEBCDRLGPGWADI 240
DB 181 PQDGPRSKPQPKDNGDVQCDCIQMVTDIQTAVRTNSTFVQALVEHVKEBCDRLGPGWADI 240

QY 241 CKNYISOYSEIAIQMMHMQPKKEICALVGFCDVEKEMPMQTLVPKAVASKNVIPAELVE 300
DB 241 CKNYISOYSEIAIQMMHMQPKKEICALVGFCDVEKEMPMQTLVPKAVASKNVIPAELVE 300

QY 301 PIKKEHVPAKSDYCEVCEFLVKEVTKLIDNNKTEKEIILDAPDKMCSKLPKSLSESCQEV 360
DB 301 PIKKEHVPAKSDYCEVCEFLVKEVTKLIDNNKTEKEIILDAPDKMCSKLPKSLSESCQEV 360

QY 361 VDTYGSIIILLEEVSPELVCSMLHLCSTRLPALTVHVTQPKDGFCEVCKLVGYLD 420
DB 361 VDTYGSIIILLEEVSPELVCSMLHLCSTRLPALTVHVTQPKDGFCEVCKLVGYLD 420

QY 421 RNLEKSTQKEILAALEKGCSEFLPDPYQKQCDQFVAEYEPVLIEILVEVMDPSFVCLKIG 480
DB 421 RNLEKSTQKEILAALEKGCSEFLPDPYQKQCDQFVAEYEPVLIEILVEVMDPSFVCLKIG 480

QY 481 ACPSAHKPLLGTEKCIWGPSYWCNTETAAQCNAVEHCKRHHVN 524
DB 481 ACPSAHKPLLGTEKCIWGPSYWCNTETAAQCNAVEHCKRHHVN 524

RESULT 6
US-10-428-817A-56
; Sequence 56, Application US/10428817A
; Publication No. US20040214783A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 38373-189118
; CURRENT APPLICATION NUMBER: US/10/428,817A
; CURRENT FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: US 60/378,988
; PRIOR FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: US 60/389,366
; PRIOR FILING DATE: 2002-06-15
; PRIOR APPLICATION NUMBER: US 60/406,697
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US 60/406,750
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/415,310
; PRIOR FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US 60/415,400
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: US 60/438,686
; PRIOR FILING DATE: 2003-01-09
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 56
; LENGTH: 524
; TYPE: PRT
```

Wed Jan 18 11:58:40 2006

ORGANISM: Homo sapiens
US-10-428-817A-56

```
Query Match      100.0%; Score 2789; DB 4; Length 524;
Best Local Similarity 100.0%; Pred. No. 1.6e-224;
Matches 524; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy	1	MYALFLLASLUGAALAGPVLGLKECTRGSAVWCNQVKTASDCCGAVKHCLQTVWNKPVTKS	60
Db	1	MYALFLLASLUGAALAGPVLGLKECTRGSAVWCNQVKTASDCCGAVKHCLQTVWNKPVTKS	60
Qy	61	LPDCIDKDVVTAAGDMLKONATEBEEILVYLEKTCDWLPKPNMSASCKEIVDSYLPVILDI	120
Db	61	LPDCIDKDVVTAAGDMLKONATEBEEILVYLEKTCDWLPKPNMSASCKEIVDSYLPVILDI	120
Qy	121	IKGEMSPGVCESALNT.CESLOKHLAEINHQKQLESNKIPELDMTEVVAPPMANIPLILLY	180
Db	121	IKGEMSPGVCESALNT.CESLOKHLAEINHQKQLESNKIPELDMTEVVAPPMANIPLILLY	180
Qy	181	PDQGPSPKPOP.KONGDVCQDCIQMVVTDIQTAVRTNSTFVQALVEHVKEECDRLGFGMADI	240
Db	181	PDQGPSPKPOP.KONGDVCQDCIQMVVTDIQTAVRTNSTFVQALVEHVKEECDRLGFGMADI	240
Qy	241	CKNVIISOYSEIAIQMMHMQPKBEICALVGFCDEVKEMPQOTLVPKAVASKNVI.PALELVE	300
Db	241	CKNVIISOYSEIAIQMMHMQPKBEICALVGFCDEVKEMPQOTLVPKAVASKNVI.PALELVE	300
Qy	301	PIKKGHEVPAKSDVYCEVCEFLVKEVTKLIDNNKTEKEILDADFDMCKSLPKSLSEECQEV	360
Db	301	PIKKGHEVPAKSDVYCEVCEFLVKEVTKLIDNNKTEKEILDADFDMCKSLPKSLSEECQEV	360
Qy	361	VDTYGSSILSILLBEVSPELVCSMLHLCSGTRLPALT.VHVVTQPKDGGFCVCKKL.VGYLD	420
Db	361	VDTYGSSILSILLBEVSPELVCSMLHLCSGTRLPALT.VHVVTQPKDGGFCVCKKL.VGYLD	420
Qy	421	RNLKFNSTKQBEILAALEKGCSEFLPDPYQKQCDQFVAEYEPVLIELVEMDPSFVCLKIG	480
Db	421	RNLKFNSTKQBEILAALEKGCSEFLPDPYQKQCDQFVAEYEPVLIELVEMDPSFVCLKIG	480
Qy	481	ACPSAHKPLLTGTEKICWGPSYWCQNTETAAQCNVAHECHKRHVN	524
Db	481	ACPSAHKPLLTGTEKICWGPSYWCQNTETAAQCNVAHECHKRHVN	524

```

RESULT 7
US-10-801-517-1
; Sequence 1, Application US/10801517
; Publication No. US20040229799A1
; GENERAL INFORMATION:
; APPLICANT: Qi, Xiaoyang
; APPLICANT: Children's Hospital Medical Center
; TITLE OF INVENTION: Sapsosin C-DOPS A Novel Anti-Tumor Agent
; FILE REFERENCE: CMI08/GN003
; CURRENT APPLICATION NUMBER: US/10/801,517
; CURRENT FILING DATE: 2004-03-16
; PRIOR APPLICATION NUMBER: 60/446,166
; PRIOR FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: SeqSERO for Windows Version 4.0

```

Query Match	100.0%;	Score 2789;	DB 5;	Length 524;
Best Local Similarity	100.0%;	Pred. No. 1.6e-224;		
Matches 524:	Conservative	0;	Mismatches 0;	Indels 0;
	Gaps	0;		

QY 1 MYAFLLASLLGAALAGPVILGLKETTRGSAVWQNVKTASDCGAVKHCLQTWNKPVTKS 60

ph 1 MYAFLLASLLGAALAGPVILGLKETTRGSAVWQNVKTASDCGAVKHCLQTWNKPVTKS 60

61	Qy	LP	CD	1	CKDVT	TAAGDMLKXNATEE	ILVY	LEK	TC	DWL	PKPNN	SA	CKE	IV	DSY	L	PV	LD	120
61	Db	LP	CD	1	CKDVT	TAAGDMLKXNATEE	ILVY	LEK	TC	DWL	PKPNN	SA	CKE	IV	DSY	L	PV	LD	120
121	Qy	IK	EMS	R	PGE	VCS	ALN	LC	ES	LQ	KH	LA	ELN	HQ	K	Q	LES	NI	180
121	Db	IK	EMS	R	PGE	VCS	ALN	LC	ES	LQ	KH	LA	ELN	HQ	K	Q	LES	NI	180
181	Qy	PD	Q	SR	S	K	P	Q	P	K	D	G	V	C	D	C	I	Q	240
181	Db	PD	Q	SR	S	K	P	Q	P	K	D	G	V	C	D	C	I	Q	240
241	Qy	CK	NY	I	S	Q	Y	S	E	I	A	I	Q	M	M	H	M	P	300
241	Db	CK	NY	I	S	Q	Y	S	E	I	A	I	Q	M	M	H	M	P	300
301	Qy	PI	K	G	H	E	V	P	A	K	S	D	V	Y	C	E	V	C	360
301	Db	PI	K	G	H	E	V	P	A	K	S	D	V	Y	C	E	V	C	360
361	Qy	VD	T	Y	G	S	S	I	L	L	E	V	S	P	E	L	V	C	420
361	Db	VD	T	Y	G	S	S	I	L	L	E	V	S	P	E	L	V	C	420
421	Qy	R	N	L	E	K	N	S	T	Q	E	I	A	L	E	K	C	S	480
421	Db	R	N	L	E	K	N	S	T	Q	E	I	A	L	E	K	C	S	480
481	Qy	A	C	P	S	A	H	K	P	L	L	G	T	E	K	C	I	W	524
481	Db	A	C	P	S	A	H	K	P	L	L	G	T	E	K	C	I	W	524

```

RESULT 8
US-10-473-127-1865
; Sequence 1865, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473, 127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1865
; LENGTH: 524
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1865

```

Query Match	100.0%;	Score 2789;	DB 5;	Length 524;
Best Local Similarity	100.0%;	Pred. No. 1.6e-224;		
Matches 524;	Conservative	0;	Mismatches 0;	Indels 0;
Gaps 0;				

Qy	1	MYAFLLASLLGAALAGPVLGLKECTRGSAVWCQNVKTASDCCGAVKHCLQTWVWVKPTVKS	60
Qy	1	MYAFLLASLLGAALAGPVLGLKECTRGSAVWCQNVKTASDCCGAVKHCLQTWVWVKPTVKS	60
Db	1	MYAFLLASLLGAALAGPVLGLKECTRGSAVWCQNVKTASDCCGAVKHCLQTWVWVKPTVKS	60
Qy	61	LPDCICKDVVTAAGDMLKONATBEELIIVYLEKTCDWLPKPNMWSASCKEIVDSYLPVLIDI	120

Db 61 LPDCICKDVVTAAGDMLKONATEBEEILVLEKTCMDLKPKNMSASCKEIVDSYLPVILDI 120
QY 121 IKGEMSRPGEVCSALNLCESLQKHLAELNHQKQLESNKIPELDMTEVAVPFMANIPLLLY 180
Db 121 IKGEMSRPGEVCSALNLCESLQKHLAELNHQKQLESNKIPELDMTEVAVPFMANIPLLLY 180
QY 181 PDGPRSKPQKONGDVQDCIQMVTDIQTAVRTNSTFVQALVHVHKBECDRLPGMADI 240
Db 181 PDGPRSKPQKONGDVQDCIQMVTDIQTAVRTNSTFVQALVHVHKBECDRLPGMADI 240
QY 241 CKNYISQYSEIAIQMMHMQPKKEICALVGFCDVEKEMPQTLVPAKVASKNVIPALELVE 300
Db 241 CKNYISQYSEIAIQMMHMQPKKEICALVGFCDVEKEMPQTLVPAKVASKNVIPALELVE 300
QY 301 PIKKEHVPAKSDVYCEVCFVKEVTKLIDNNKTEKEIILDAFDMCKSKLPKSLSEBCEQV 360
Db 301 PIKKEHVPAKSDVYCEVCFVKEVTKLIDNNKTEKEIILDAFDMCKSKLPKSLSEBCEQV 360
QY 361 VDTYGSLSILLESVSPPELVCSMLHLCSTGTRLPALTUVHTQPKDGGFCEVCKKLVGYLD 420
Db 361 VDTYGSLSILLESVSPPELVCSMLHLCSTGTRLPALTUVHTQPKDGGFCEVCKKLVGYLD 420
QY 421 RNLEKNSTQKEIILAALKEGCSFLPDYPYQKQCDQFVAEYEPVLIEILVEVMDPSFVCLKIG 480
Db 421 RNLEKNSTQKEIILAALKEGCSFLPDYPYQKQCDQFVAEYEPVLIEILVEVMDPSFVCLKIG 480
QY 481 ACPSAHKPLLGTEKCIWGPSYWCNTETAACNAVEHCRRHVN 524
Db 481 ACPSAHKPLLGTEKCIWGPSYWCNTETAACNAVEHCRRHVN 524

RESULT 9

US-10-473-127-1866
; Sequence 1866, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1866
; LENGTH: 524
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1866

Query Match 100.0%; Score 2789; DB 5; Length 524;
Best Local Similarity 100.0%; Pred. No. 1.6e-224;
Matches 524; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MYALFLLASLLGAALAGPVILGKECTRGSAVWQNVKTASDCGAVKHCLQTVWNKPTVKS 60
Db 1 MYALFLLASLLGAALAGPVILGKECTRGSAVWQNVKTASDCGAVKHCLQTVWNKPTVKS 60
QY 61 LPDCICKDVVTAAGDMLKONATEBEEILVLEKTCMDLKPKNMSASCKEIVDSYLPVILDI 120
Db 61 LPDCICKDVVTAAGDMLKONATEBEEILVLEKTCMDLKPKNMSASCKEIVDSYLPVILDI 120

QY 121 IKGEMSRPGEVCSALNLCESLQKHLAELNHQKQLESNKIPELDMTEVAVPFMANIPLLLY 180
Db 121 IKGEMSRPGEVCSALNLCESLQKHLAELNHQKQLESNKIPELDMTEVAVPFMANIPLLLY 180
QY 181 PDGPRSKPQKONGDVQDCIQMVTDIQTAVRTNSTFVQALVHVHKBECDRLPGMADI 240
Db 181 PDGPRSKPQKONGDVQDCIQMVTDIQTAVRTNSTFVQALVHVHKBECDRLPGMADI 240
QY 241 CKNYISQYSEIAIQMMHMQPKKEICALVGFCDVEKEMPQTLVPAKVASKNVIPALELVE 300
Db 241 CKNYISQYSEIAIQMMHMQPKKEICALVGFCDVEKEMPQTLVPAKVASKNVIPALELVE 300
QY 301 PIKKEHVPAKSDVYCEVCFVKEVTKLIDNNKTEKEIILDAFDMCKSKLPKSLSEBCEQV 360
Db 301 PIKKEHVPAKSDVYCEVCFVKEVTKLIDNNKTEKEIILDAFDMCKSKLPKSLSEBCEQV 360
QY 361 VDTYGSLSILLESVSPPELVCSMLHLCSTGTRLPALTUVHTQPKDGGFCEVCKKLVGYLD 420
Db 361 VDTYGSLSILLESVSPPELVCSMLHLCSTGTRLPALTUVHTQPKDGGFCEVCKKLVGYLD 420
QY 421 RNLEKNSTQKEIILAALKEGCSFLPDYPYQKQCDQFVAEYEPVLIEILVEVMDPSFVCLKIG 480
Db 421 RNLEKNSTQKEIILAALKEGCSFLPDYPYQKQCDQFVAEYEPVLIEILVEVMDPSFVCLKIG 480
QY 481 ACPSAHKPLLGTEKCIWGPSYWCNTETAACNAVEHCRRHVN 524
Db 481 ACPSAHKPLLGTEKCIWGPSYWCNTETAACNAVEHCRRHVN 524

RESULT 10

US-10-473-127-1868
; Sequence 1868, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1868
; LENGTH: 524
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1868

Query Match 100.0%; Score 2789; DB 5; Length 524;
Best Local Similarity 100.0%; Pred. No. 1.6e-224;
Matches 524; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYALFLLASLLGAALAGPVILGKECTRGSAVWQNVKTASDCGAVKHCLQTVWNKPTVKS 60
Db 1 MYALFLLASLLGAALAGPVILGKECTRGSAVWQNVKTASDCGAVKHCLQTVWNKPTVKS 60
QY 61 LPDCICKDVVTAAGDMLKONATEBEEILVLEKTCMDLKPKNMSASCKEIVDSYLPVILDI 120
Db 61 LPDCICKDVVTAAGDMLKONATEBEEILVLEKTCMDLKPKNMSASCKEIVDSYLPVILDI 120
QY 121 IKGEMSRPGEVCSALNLCESLQKHLAELNHQKQLESNKIPELDMTEVAVPFMANIPLLLY 180

Db	121	IKGMSRPGVCSALNLCESLQKHLAELNHQKQLESNKIPELDMTEVAPFMANIPILLY	180
Qy	181	PDGPRSKPQKONGDVQCDCIQMVTDIQTAVRTNSTFVQALVEHVKEECDRLGPGWADI	240
Db	181	PDGPRSKPQKONGDVQCDCIQMVTDIQTAVRTNSTFVQALVEHVKEECDRLGPGWADI	240
Qy	241	CKNYISQYSEIATQMMHMQPKIEICALVGFCDVEKEMPMTQLVPAKVASKNVIPALSELVE	300
Db	241	CKNYISQYSEIATQMMHMQPKIEICALVGFCDVEKEMPMTQLVPAKVASKNVIPALSELVE	300
Qy	301	PIKKEHPAKSDVYCEVCEFLVKEVTKLIDNNKTEKIELDAFDMCKSKLPKSLSEECQEV	360
Db	301	PIKKEHPAKSDVYCEVCEFLVKEVTKLIDNNKTEKIELDAFDMCKSKLPKSLSEECQEV	360
Qy	361	VDYTGSSILSLLEVSPELVCSMLHLCSTGRLPALTVHVTQPKDGGFCEVCKKLVGYLD	420
Db	361	VDYTGSSILSLLEVSPELVCSMLHLCSTGRLPALTVHVTQPKDGGFCEVCKKLVGYLD	420
Qy	421	RNLEKNSTKQIEILAALEKGCFLPDPYQKQCDQFVAEYEPVLIEILVEVMDPSFVCLKIG	480
Db	421	RNLEKNSTKQIEILAALEKGCFLPDPYQKQCDQFVAEYEPVLIEILVEVMDPSFVCLKIG	480
Qy	481	ACPSAHKPLLGTEKICINGPSYWCQNTETAACNAVEHCKRHVN	524
Db	481	ACPSAHKPLLGTEKICINGPSYWCQNTETAACNAVEHCKRHVN	524
RESULT 11			
US-10-473-127-1869			
; Sequence 1869, Application US/10473127			
; Publication No. US20040236091A1			
; GENERAL INFORMATION:			
; APPLICANT: Zycos Inc.			
; TITLE OF INVENTION: TRANSLATIONAL PROFILING			
; FILE REFERENCE: 08191-026W01			
; CURRENT APPLICATION NUMBER: US/10/473,127			
; CURRENT FILING DATE: 2003-09-26			
; PRIOR APPLICATION NUMBER: 60/279,495			
; PRIOR FILING DATE: 2001-03-28			
; PRIOR APPLICATION NUMBER: 60/292,544			
; PRIOR FILING DATE: 2001-05-21			
; PRIOR APPLICATION NUMBER: 60/310,801			
; PRIOR FILING DATE: 2001-08-08			
; PRIOR APPLICATION NUMBER: 60/326,370			
; PRIOR FILING DATE: 2001-10-01			
; PRIOR APPLICATION NUMBER: 60/336,780			
; PRIOR FILING DATE: 2001-12-04			
; PRIOR APPLICATION NUMBER: 60/358,985			
; PRIOR FILING DATE: 2002-02-20			
; NUMBER OF SEQ ID NOS: 2041			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 1869			
; LENGTH: 524			
; TYPE: PRT			
; ORGANISM: Homo sapiens			
US-10-473-127-1869			
Query Match 100.0%; Score 2789; DB 5; Length 524;			
Best Local Similarity 100.0%; Pred. No. 1.6e-224;			
Matches 524; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1	MYAFLLASLLGAALAGPVILGKECTRGSAVWQNVKTASDCGAVKHGCLQTVWNKPTVKS	60
Db	1	MYAFLLASLLGAALAGPVILGKECTRGSAVWQNVKTASDCGAVKHGCLQTVWNKPTVKS	60
Qy	61	LPDCICKDVVTAAGDMLKDNATEEILVYLEKTCMDLKPKNMSASCKEIVDSYLPVILDI	120
Db	61	LPDCICKDVVTAAGDMLKDNATEEILVYLEKTCMDLKPKNMSASCKEIVDSYLPVILDI	120
Qy	121	IKGMSRPGVCSALNLCESLQKHLAELNHQKQLESNKIPELDMTEVAPFMANIPILLY	180
Db	121	IKGMSRPGVCSALNLCESLQKHLAELNHQKQLESNKIPELDMTEVAPFMANIPILLY	180
Qy	181	PDGPRSKPQKONGDVQCDCIQMVTDIQTAVRTNSTFVQALVEHVKEECDRLGPGWADI	240
Db	181	PDGPRSKPQKONGDVQCDCIQMVTDIQTAVRTNSTFVQALVEHVKEECDRLGPGWADI	240

Qy	181	PDGPRSKPQKONGDVQCDCIQMVTDIQTAVRTNSTFVQALVEHVKEECDRLGPGWADI	240
Db	181	PDGPRSKPQKONGDVQCDCIQMVTDIQTAVRTNSTFVQALVEHVKEECDRLGPGWADI	240
Qy	241	CKNYISQYSEIATQMMHMQPKIEICALVGFCDVEKEMPMTQLVPAKVASKNVIPALSELVE	300
Db	241	CKNYISQYSEIATQMMHMQPKIEICALVGFCDVEKEMPMTQLVPAKVASKNVIPALSELVE	300
Qy	301	PIKKEHPAKSDVYCEVCEFLVKEVTKLIDNNKTEKIELDAFDMCKSKLPKSLSEECQEV	360
Db	301	PIKKEHPAKSDVYCEVCEFLVKEVTKLIDNNKTEKIELDAFDMCKSKLPKSLSEECQEV	360
Qy	361	VDYTGSSILSLLEVSPELVCSMLHLCSTGRLPALTVHVTQPKDGGFCEVCKKLVGYLD	420
Db	361	VDYTGSSILSLLEVSPELVCSMLHLCSTGRLPALTVHVTQPKDGGFCEVCKKLVGYLD	420
Qy	421	RNLEKNSTKQIEILAALEKGCFLPDPYQKQCDQFVAEYEPVLIEILVEVMDPSFVCLKIG	480
Db	421	RNLEKNSTKQIEILAALEKGCFLPDPYQKQCDQFVAEYEPVLIEILVEVMDPSFVCLKIG	480
Qy	481	ACPSAHKPLLGTEKICINGPSYWCQNTETAACNAVEHCKRHVN	524
Db	481	ACPSAHKPLLGTEKICINGPSYWCQNTETAACNAVEHCKRHVN	524
RESULT 12			
US-10-473-127-1871			
; Sequence 1871, Application US/10473127			
; Publication No. US20040236091A1			
; GENERAL INFORMATION:			
; APPLICANT: Zycos Inc.			
; TITLE OF INVENTION: TRANSLATIONAL PROFILING			
; FILE REFERENCE: 08191-026W01			
; CURRENT APPLICATION NUMBER: US/10/473,127			
; CURRENT FILING DATE: 2003-09-26			
; PRIOR APPLICATION NUMBER: 60/279,495			
; PRIOR FILING DATE: 2001-03-28			
; PRIOR APPLICATION NUMBER: 60/292,544			
; PRIOR FILING DATE: 2001-05-21			
; PRIOR APPLICATION NUMBER: 60/310,801			
; PRIOR FILING DATE: 2001-08-08			
; PRIOR APPLICATION NUMBER: 60/326,370			
; PRIOR FILING DATE: 2001-10-01			
; PRIOR APPLICATION NUMBER: 60/336,780			
; PRIOR FILING DATE: 2001-12-04			
; PRIOR APPLICATION NUMBER: 60/358,985			
; PRIOR FILING DATE: 2002-02-20			
; NUMBER OF SEQ ID NOS: 2041			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 1871			
; LENGTH: 524			
; TYPE: PRT			
; ORGANISM: Homo sapiens			
US-10-473-127-1871			
Query Match 100.0%; Score 2789; DB 5; Length 524;			
Best Local Similarity 100.0%; Pred. No. 1.6e-224;			
Matches 524; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1	MYAFLLASLLGAALAGPVILGKECTRGSAVWQNVKTASDCGAVKHGCLQTVWNKPTVKS	60
Db	1	MYAFLLASLLGAALAGPVILGKECTRGSAVWQNVKTASDCGAVKHGCLQTVWNKPTVKS	60
Qy	61	LPDCICKDVVTAAGDMLKDNATEEILVYLEKTCMDLKPKNMSASCKEIVDSYLPVILDI	120
Db	61	LPDCICKDVVTAAGDMLKDNATEEILVYLEKTCMDLKPKNMSASCKEIVDSYLPVILDI	120
Qy	121	IKGMSRPGVCSALNLCESLQKHLAELNHQKQLESNKIPELDMTEVAPFMANIPILLY	180
Db	121	IKGMSRPGVCSALNLCESLQKHLAELNHQKQLESNKIPELDMTEVAPFMANIPILLY	180
Qy	181	PDGPRSKPQKONGDVQCDCIQMVTDIQTAVRTNSTFVQALVEHVKEECDRLGPGWADI	240
Db	181	PDGPRSKPQKONGDVQCDCIQMVTDIQTAVRTNSTFVQALVEHVKEECDRLGPGWADI	240

Db 181 PQDGRSKPQKONGDVQCDCIQMVTDTQTAVRTNSTFVQALVEHVKECDRLGPGMADI 240
Qy 241 CKNYISQYSIAIQMMHMQPKIEICALVGFCDVEKEMPOTTLVPAKVASKNVIPALELVE 300
Db 241 CKNYISQYSIAIQMMHMQPKIEICALVGFCDVEKEMPOTTLVPAKVASKNVIPALELVE 300
Qy 301 PIKKEHVPKSDVYCEVCEFLVKEVTKLIDNNKTEKEILDADFKMCKSLPKSLSEBCEV 360
Db 301 PIKKEHVPKSDVYCEVCEFLVKEVTKLIDNNKTEKEILDADFKMCKSLPKSLSEBCEV 360
Qy 361 VDTYSSILSILLEEVSPELVCSMLHLCSTGTRLPALTTHVTQPKDGGFCFCEVCKLVGYLD 420
Db 361 VDTYSSILSILLEEVSPELVCSMLHLCSTGTRLPALTTHVTQPKDGGFCFCEVCKLVGYLD 420
Qy 421 RNLEKNSTQKEILAALEKGCFLPDPYQKQCDQFVAEYEPVLIEILVEVMDPSFVCLKIG 480
Db 421 RNLEKNSTQKEILAALEKGCFLPDPYQKQCDQFVAEYEPVLIEILVEVMDPSFVCLKIG 480
Qy 481 ACPSAHKPLLGTEKCIWGPSYWCNTETAACQNAVEHCKRHWVN 524
Db 481 ACPSAHKPLLGTEKCIWGPSYWCNTETAACQNAVEHCKRHWVN 524

RESULT 13

US-10-473-127-1873
; Sequence 1873, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; PRIOR FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1873
; LENGTH: 524
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-473-127-1873

Query Match 100.0%; Score 2789; DB 5; Length 524;
Best Local Similarity 100.0%; Pred. No. 1.6e-224;
Matches 524; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MYALFLASLLGAAAGPVLGLKECTRGSAVWCNVKTASDCGAVKHCLQTVWNKPTVKS 60
Db 1 MYALFLASLLGAAAGPVLGLKECTRGSAVWCNVKTASDCGAVKHCLQTVWNKPTVKS 60
Qy 61 LPCDICKDVTAAAGDMLKDNATEEILVYLEKTCMDLPKPNMSASCKEIVDSYLPVLDI 120
Db 61 LPCDICKDVTAAAGDMLKDNATEEILVYLEKTCMDLPKPNMSASCKEIVDSYLPVLDI 120
Qy 121 IKGMSRPGVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVAVPFMANIPILLY 180
Db 121 IKGMSRPGVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVAVPFMANIPILLY 180
Qy 181 PQDGRSKPQKONGDVQCDCIQMVTDTQTAVRTNSTFVQALVEHVKECDRLGPGMADI 240
Db 181 PQDGRSKPQKONGDVQCDCIQMVTDTQTAVRTNSTFVQALVEHVKECDRLGPGMADI 240

Qy 241 CKNYISQYSIAIQMMHMQPKIEICALVGFCDVEKEMPOTTLVPAKVASKNVIPALELVE 300
Db 241 CKNYISQYSIAIQMMHMQPKIEICALVGFCDVEKEMPOTTLVPAKVASKNVIPALELVE 300
Qy 301 PIKKEHVPKSDVYCEVCEFLVKEVTKLIDNNKTEKEILDADFKMCKSLPKSLSEBCEV 360
Db 301 PIKKEHVPKSDVYCEVCEFLVKEVTKLIDNNKTEKEILDADFKMCKSLPKSLSEBCEV 360
Qy 361 VDTYSSILSILLEEVSPELVCSMLHLCSTGTRLPALTTHVTQPKDGGFCFCEVCKLVGYLD 420
Db 361 VDTYSSILSILLEEVSPELVCSMLHLCSTGTRLPALTTHVTQPKDGGFCFCEVCKLVGYLD 420
Qy 421 RNLEKNSTQKEILAALEKGCFLPDPYQKQCDQFVAEYEPVLIEILVEVMDPSFVCLKIG 480
Db 421 RNLEKNSTQKEILAALEKGCFLPDPYQKQCDQFVAEYEPVLIEILVEVMDPSFVCLKIG 480
Qy 481 ACPSAHKPLLGTEKCIWGPSYWCNTETAACQNAVEHCKRHWVN 524
Db 481 ACPSAHKPLLGTEKCIWGPSYWCNTETAACQNAVEHCKRHWVN 524

RESULT 14

US-10-473-127-1878
; Sequence 1878, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; PRIOR FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1878
; LENGTH: 524
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-473-127-1878

Query Match 100.0%; Score 2789; DB 5; Length 524;
Best Local Similarity 100.0%; Pred. No. 1.6e-224;
Matches 524; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MYALFLASLLGAAAGPVLGLKECTRGSAVWCNVKTASDCGAVKHCLQTVWNKPTVKS 60
Db 1 MYALFLASLLGAAAGPVLGLKECTRGSAVWCNVKTASDCGAVKHCLQTVWNKPTVKS 60
Qy 61 LPCDICKDVTAAAGDMLKDNATEEILVYLEKTCMDLPKPNMSASCKEIVDSYLPVLDI 120
Db 61 LPCDICKDVTAAAGDMLKDNATEEILVYLEKTCMDLPKPNMSASCKEIVDSYLPVLDI 120
Qy 121 IKGMSRPGVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVAVPFMANIPILLY 180
Db 121 IKGMSRPGVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVAVPFMANIPILLY 180
Qy 181 PQDGRSKPQKONGDVQCDCIQMVTDTQTAVRTNSTFVQALVEHVKECDRLGPGMADI 240
Db 181 PQDGRSKPQKONGDVQCDCIQMVTDTQTAVRTNSTFVQALVEHVKECDRLGPGMADI 240
Qy 241 CKNYISQYSIAIQMMHMQPKIEICALVGFCDVEKEMPOTTLVPAKVASKNVIPALELVE 300

Db 241 CKNYISQYSEIAIQMMHMQPKETICALVGFCDVEKEMPMQTLVPAKASKNVIIPALELVE 300
Qy 301 PIKKHEVPAKSDVYCEVCEFLVKEVTCLIINNKTKEILDADFDMKCSKLPKSLSEECQEV 360
Db 301 PIKKHEVPAKSDVYCEVCEFLVKEVTCLIINNKTKEILDADFDMKCSKLPKSLSEECQEV 360
Qy 361 VDTYGSSILSILLBEVSPELVCSMLHLCSGTRLPALTVHVTQPKDGGFCVCKKLVGYLD 420
Db 361 VDTYGSSILSILLBEVSPELVCSMLHLCSGTRLPALTVHVTQPKDGGFCVCKKLVGYLD 420
Qy 421 RNLEKNSTKQRIILAEKGCFLPDYQKQCDQFVAEYEPVLIIRILVEVMDPSFVCLKIG 480
Db 421 RNLEKNSTKQRIILAEKGCFLPDYQKQCDQFVAEYEPVLIIRILVEVMDPSFVCLKIG 480
Qy 481 ACPSAHKPLLGTEKCIWGPSYWCNTETAACNAVEHCKRHVWN 524
Db 481 ACPSAHKPLLGTEKCIWGPSYWCNTETAACNAVEHCKRHVWN 524

RESULT 15
US-10-473-127-1879
; Sequence 1879, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1879
; LENGTH: 524
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1879

Query Match 100.0%; Score 2789; DB 5; Length 524;
Best Local Similarity 100.0%; Pred. No. 1.6e-224;
Matches 524; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MYALFLLASLLGAALAGPVGLKECTRGSAVWQNVKTASDCGAVKHCLQTWNKPTVKS 60
Db 1 MYALFLLASLLGAALAGPVGLKECTRGSAVWQNVKTASDCGAVKHCLQTWNKPTVKS 60
Qy 61 LPCDICKQVVTAGDMKDNATEERTLVYLEKTCDWLPKPNMSASCKEIVDSYLPVILDI 120
Db 61 LPCDICKQVVTAGDMKDNATEERTLVYLEKTCDWLPKPNMSASCKEIVDSYLPVILDI 120
Qy 121 IKGEMSRPGEVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVVAFFMANIPLLLY 180
Db 121 IKGEMSRPGEVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVVAFFMANIPLLLY 180
Qy 181 PQDGRSKPQKONGDVQDCIQMVTDIQTAVRTNSTFVQALVEHVKEECDRLGFQMADI 240
Db 181 PQDGRSKPQKONGDVQDCIQMVTDIQTAVRTNSTFVQALVEHVKEECDRLGFQMADI 240
Qy 241 CKNYISQYSEIAIQMMHMQPKETICALVGFCDVEKEMPMQTLVPAKASKNVIIPALELVE 300
Db 241 CKNYISQYSEIAIQMMHMQPKETICALVGFCDVEKEMPMQTLVPAKASKNVIIPALELVE 300

Qy 301 PIKKHEVPAKSDVYCEVCEFLVKEVTCLIINNKTKEILDADFDMKCSKLPKSLSEECQEV 360
Db 301 PIKKHEVPAKSDVYCEVCEFLVKEVTCLIINNKTKEILDADFDMKCSKLPKSLSEECQEV 360
Qy 361 VDTYGSSILSILLBEVSPELVCSMLHLCSGTRLPALTVHVTQPKDGGFCVCKKLVGYLD 420
Db 361 VDTYGSSILSILLBEVSPELVCSMLHLCSGTRLPALTVHVTQPKDGGFCVCKKLVGYLD 420
Qy 421 RNLEKNSTKQRIILAEKGCFLPDYQKQCDQFVAEYEPVLIIRILVEVMDPSFVCLKIG 480
Db 421 RNLEKNSTKQRIILAEKGCFLPDYQKQCDQFVAEYEPVLIIRILVEVMDPSFVCLKIG 480
Qy 481 ACPSAHKPLLGTEKCIWGPSYWCNTETAACNAVEHCKRHVWN 524
Db 481 ACPSAHKPLLGTEKCIWGPSYWCNTETAACNAVEHCKRHVWN 524

Search completed: January 13, 2006, 16:38:41
Job time : 101.768 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2006, Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 13, 2006, 16:30:30 ; Search time 10.4106 Seconds
(without alignments)
475.862 Million cell updates/sec

Title: US-10-801-517-1

Perfect score: 2789

Sequence: 1 MYALFLLASLLGALAGPVL.....NTETRAQCNVAHECKRHVWN 524

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 67062 seqs, 9454214 residues

Total number of hits satisfying chosen parameters: 67062

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA New.*

- 1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2789	100.0	524	6	US-10-821-234-1631
2	113.5	4.1	3803	6	US-10-995-561-773
3	113.5	4.1	3960	6	US-10-995-561-771
4	113.5	4.1	5335	6	US-10-995-561-777
5	113.5	4.1	5406	6	US-10-995-561-774
6	113.5	4.1	5415	6	US-10-995-561-779
7	113.5	4.1	5464	6	US-10-995-561-775
8	113	4.1	1786	7	US-11-196-400-3
9	108.5	3.9	3674	7	US-11-000-463-454
10	107.5	3.9	2036	7	US-11-124-368A-276
11	107.5	3.9	2036	7	US-11-124-368A-280
12	107.5	3.9	2036	7	US-11-124-368A-281
13	107.5	3.9	2044	7	US-11-124-368A-278
14	107.5	3.9	2144	7	US-11-124-368A-277
15	102	3.7	630	7	US-11-186-400-5
16	101	3.6	989	6	US-10-821-234-975
17	98.5	3.5	1404	6	US-10-878-556A-169
18	96.5	3.5	413	6	US-10-821-234-989
19	96	3.4	574	6	US-10-518-341-1
20	96	3.4	574	7	US-11-022-562-214
21	96	3.4	1062	7	US-11-137-465-43
22	95.5	3.4	469	7	US-11-124-368A-321
23	94	3.4	476	6	US-10-878-556A-158
24	94	3.4	585	6	US-10-821-234-875
25	93.5	3.4	782	7	US-11-145-631-9

26	93.5	3.4	930	6	US-10-821-234-1188	Sequence 1188, Ap
27	93.5	3.4	5935	6	US-10-995-561-776	Sequence 776, App
28	93	3.3	3002	6	US-10-821-234-916	Sequence 916, App
29	92.5	3.3	754	6	US-10-467-962B-63	Sequence 63, Appli
30	92.5	3.3	1163	7	US-11-044-899-2	Sequence 2, Appli
31	92.5	3.3	1163	7	US-11-044-899-30	Sequence 30, Appli
32	90.5	3.2	459	6	US-10-763-712A-70	Sequence 70, Appli
33	90.5	3.2	503	6	US-10-878-556A-2	Sequence 2, Appli
34	90.5	3.2	537	6	US-10-821-234-1427	Sequence 1427, Ap
35	90.5	3.2	741	7	US-11-191-374-18	Sequence 18, Appli
36	90.5	3.2	741	7	US-11-191-375-18	Sequence 18, Appli
37	90.5	3.2	741	7	US-11-191-588-18	Sequence 18, Appli
38	90.5	3.2	1586	6	US-10-821-234-901	Sequence 901, App
39	90.5	3.2	2048	7	US-11-116-939-6	Sequence 6, Appli
40	89.5	3.2	420	6	US-10-131-826A-290	Sequence 290, App
41	89.5	3.2	618	6	US-10-523-912-4	Sequence 4, Appli
42	89.5	3.2	1933	6	US-10-523-912-2	Sequence 2, Appli
43	89.5	3.2	5024	6	US-10-793-626-2964	Sequence 2964, Ap
44	89	3.2	556	6	US-10-995-561-766	Sequence 766, App
45	89	3.2	556	6	US-10-995-561-767	Sequence 767, App

ALIGNMENTS

RESULT 1
US-10-821-234-1631
; Sequence 1631, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Grain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pc SEQ_genes Version 1.0
; SEQ ID NO 1631
; LENGTH: 524
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1631

Query Match	100.0%;	Score 2789;	DB 6;	Length 524;
Best Local Similarity	100.0%;	Pred. No. 4e-211;		
Matches 524;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MYALFLLASLLGALAGPVLGLKECTRGSAVWQNVKTASDCCGAVKHCLQTVWVKPTVKS	60	
DB	1	MYALFLLASLLGALAGPVLGLKECTRGSAVWQNVKTASDCCGAVKHCLQTVWVKPTVKS	60	
QY	61	LPDCICKDVVTRAGDMLKDNATEEELVYLEKTCMDLPKNMSASCKEIVDSYLPVLIDI	120	
DB	61	LPDCICKDVVTRAGDMLKDNATEEELVYLEKTCMDLPKNMSASCKEIVDSYLPVLIDI	120	
QY	121	IKGEMSRPGEVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVVAFFPMANIPILLY	180	
DB	121	IKGEMSRPGEVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVVAFFPMANIPILLY	180	
QY	181	PDGPRSKPQPKNGDVQCDICIMVTDIQTAVRTNSTFVQALVHVHKEECDRLPGMADI	240	
DB	181	PDGPRSKPQPKNGDVQCDICIMVTDIQTAVRTNSTFVQALVHVHKEECDRLPGMADI	240	
QY	241	CKNYISQYSEIATOMMMHMQPKEICALVGFCDVEKMPQTLVPAKVASKNVPALLEVE	300	
DB	241	CKNYISQYSEIATOMMMHMQPKEICALVGFCDVEKMPQTLVPAKVASKNVPALLEVE	300	
QY	301	PIKHEVPAKSDVYCEVCEFLVKEVTKLIDNNKTEKELIDAFDKMCSKLPKSLSECEQEV	360	

```

Db      301  |||||PIKKEHPAKSDVYCEVFLVKEVTKLIDNNKTEKEILDADKWCCKLPSLSECEV 360
Qy      361  VDTYSSILSLLEEVSELCVSMHLCSGTRLPALTVHVTPQKGGFCVCKKLVGLD 420
Db      361  VDTYSSILSLLEEVSELCVSMHLCSGTRLPALTVHVTPQKGGFCVCKKLVGLD 420
Qy      421  RNLEKNSKQIBLAALKEGCSFLPDYQKQCDQFVAEYEPVLIILVEMDPSFVCLKIG 480
Db      421  RNLEKNSKQIBLAALKEGCSFLPDYQKQCDQFVAEYEPVLIILVEMDPSFVCLKIG 480
Qy      481  ACPSAHKELLGTEKICWGPSYWCQNTETAACQNAVEHCKRHVN 524
Db      481  ACPSAHKELLGTEKICWGPSYWCQNTETAACQNAVEHCKRHVN 524

```

```

RESULT* 2
US-10-995-561-773
; Sequence 773, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 773
; LENGTH: 3803
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-773

```

```

Query Match      4.1%; Score 113.5; DB 6; Length 3803;
Best Local Similarity 16.3%; Pred. No. 1.4;
Matches 80; Conservative 88; Mismatches 191; Indels 133; Gaps 19;

Qy      71  TAAGDMLKDNATEEB-----ILVYLEKTCDWLPKPNMSASCKEIVDSYLPVIL 118
Db      1295 TAQEMMKPGQAEADSRVLSQSLSOOTALFAERIERNQTKLDQ-----CQKFSQQYSTIVK 1348
Qy      119  D-----IIKGEMSRPGVCSALNLCESLQKHLAEL-----NHQKQL-- 154
Db      1349 DYELQMTYKAFVESQOKSPGRRRLSSSDAITQEFMDLTRYALTTLTQHVKYISD 1408
Qy      155  -----ESNKIPE---LDMTEVVAPFMANIPLLLYPQDGRPSKPQKONGDV----- 197
Db      1409 ALRLEEEKVEEKEQHEVKEKLGWVSTLARNTQKATSETKSTDIKAILQQ 1468
Qy      198  --CQDCIQMVTDIQTAVRTNSTFVQALVEH-----VKECDRLPGFMADICKNY 244
Db      1469 VLSELTTKKEQVSEAIKTSQIF---LAKHGKLSKEKKQISEQLNALNKAYHDLCDGS 1525
Qy      245  ISQYSEIAIQM-----MMHMQPKIECALVGFCDVEVKEMPQTLVPAKVASK 290
Db      1526 ANOLOQSQLAHQTEQKTLQKQNTCHQOLEDLCSWYGOAERA-----LAGH 1573
Qy      291  NVIPALELVEPIKKEHVPK---SDVYCEVCF--LVKEVTKLIDNNKTE---KEILDAF 342
Db      1574 QGRTTQODLSALQKNSDLKDQDDIQNRATSFATVVKDIEGFMEENQTKLSPRELTALR 1633
Qy      343  DKM--CSKLPKSLSECEQVVDYSSILSILEEVSPELVCSMLHLCSGTRLPALTVHV 400
Db      1634 EKLHQAEQYALQEBETVAQKELEAVTSALQOETEKSKAAKEL--AENKKIDALLDWV 1692
Qy      401  TQPKDGGFCVCKKLVGLDRNLKNSKQIBLAALKEGC-----SFLPDPYQKQ 450
Db      1693 TSVGSSG-----GQLLTNLP--GMEQLSGASLEKGLDITTDGYMGVNOAPEKLDQK 1741
Qy      451  CQDFVAEYEPVL 462

```

```

Db      1742 CEMMKARHQELL 1753

RESULT 3
US-10-995-561-771
; Sequence 771, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 771
; LENGTH: 3960
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-771

```

```

Query Match      4.1%; Score 113.5; DB 6; Length 3960;
Best Local Similarity 16.3%; Pred. No. 1.4;
Matches 80; Conservative 88; Mismatches 191; Indels 133; Gaps 19;

Qy      71  TAAGDMLKDNATEEB-----ILVYLEKTCDWLPKPNMSASCKEIVDSYLPVIL 118
Db      1295 TAQEMMKPGQAEADSRVLSQSLSOOTALFAERIERNQTKLDQ-----CQKFSQQYSTIVK 1348
Qy      119  D-----IIKGEMSRPGVCSALNLCESLQKHLAEL-----NHQKQL-- 154
Db      1349 DYELQMTYKAFVESQOKSPGRRRLSSSDAITQEFMDLTRYALTTLTQHVKYISD 1408
Qy      155  -----ESNKIPE---LDMTEVVAPFMANIPLLLYPQDGRPSKPQKONGDV----- 197
Db      1409 ALRLEEEKVEEKEQHEVKEKLGWVSTLARNTQKATSETKSTDIKAILQQ 1468
Qy      198  --CQDCIQMVTDIQTAVRTNSTFVQALVEH-----VKECDRLPGFMADICKNY 244
Db      1469 VLSELTTKKEQVSEAIKTSQIF---LAKHGKLSKEKKQISEQLNALNKAYHDLCDGS 1525
Qy      245  ISQYSEIAIQM-----MMHMQPKIECALVGFCDVEVKEMPQTLVPAKVASK 290
Db      1526 ANOLOQSQLAHQTEQKTLQKQNTCHQOLEDLCSWYGOAERA-----LAGH 1573
Qy      291  NVIPALELVEPIKKEHVPK---SDVYCEVCF--LVKEVTKLIDNNKTE---KEILDAF 342
Db      1574 QGRTTQODLSALQKNSDLKDQDDIQNRATSFATVVKDIEGFMEENQTKLSPRELTALR 1633
Qy      343  DKM--CSKLPKSLSECEQVVDYSSILSILEEVSPELVCSMLHLCSGTRLPALTVHV 400
Db      1634 EKLHQAEQYALQEBETVAQKELEAVTSALQOETEKSKAAKEL--AENKKIDALLDWV 1692
Qy      401  TQPKDGGFCVCKKLVGLDRNLKNSKQIBLAALKEGC-----SFLPDPYQKQ 450
Db      1693 TSVGSSG-----GQLLTNLP--GMEQLSGASLEKGLDITTDGYMGVNOAPEKLDQK 1741
Qy      451  CQDFVAEYEPVL 462

```

```

RESULT 4
US-10-995-561-777
; Sequence 777, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF

```

```

, TITLE OF INVENTION, DETECTION AND USES THEREOF
,
, FILE REFERENCE: CL001559
, CURRENT APPLICATION NUMBER: US/10/995.561
, CURRENT FILING DATE: 2004-11-24
, NUMBER OF SEQ ID NOS: 85702
, SOFTWARE: FastSEQ for Windows Version 4.0
, SEQ ID NO 777
, LENGTH: 5335
, TYPE: PRT
, ORGANISM: Homo sapiens
US-10-995-561-777

```

[illegible]

```

RESULT 5
US-10-995-561-774
; Sequence 774, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: PaatSEQ for Windows Version 4.0
; SEQ ID NO 774
; LENGTH: 5406
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-774

```

Query Match	4.1%	Score 113.5	DB 6	Length 5406	
Best Local Similarity	16.3%	Pred. No. 2.1			
Matches	80	Conservative	88	Mismatches 191; Indels 133; Gaps 19	
Qy	71	TAAGDMLKONATREE-----	ILVLEKTCDWLPKPNWSASCKEIVDSYLPVIL	118	
Db	1295	TAQEMMKPGQABDSRVLSQQLSQOTAFABIERNOTKLDQ-----	CKFSQOQSYTIVK	1348	
Qy	119	D-----	IIKGEMSRPGVCSALNLCESQKHLAEI-----	NHOKQL-----	154
Db	1349	DYELQLMTYKAFVESQOKSPGKRRMLSSDAITQEFMDLRTRYALTVLTTQHVKYISD	1408		
Qy	155	-----ESNKIPE-----	LDWTEVVAPFMANIPLLLYPQDGRSPKQPKONGDV-----	197	
Db	1409	ALRRLEEEKVVEEEKQEHVEKVELLGGWSTLTARNTQKATSETKSTEDIEKAILLEEQ	1468		
Qy	198	--QDCQIQWTDIQTAVRTNSTVFQALVEH-----	VKEECDRLGPGHADICKNY	244	
Db	1469	VLSEELTTKKEQVSEAIKTSQIF--	LAKHGHKLSEKKEKQISEQLNALNKAYHDLCDGS	1525	
Qy	245	ISOVSEIAIQW-----	NMHMOPKEICALVGFCDEVKEMPMTLVPKAVASK	290	
Db	1526	ANQLQQLQSALQHTQKTLQKQNTCHQOLEDLCSWVGQAERA-----	LACH	1573	
Qy	291	NVIPALELVEPIKKEHVPAPK-----	SDVYCEVCEP--LVKEVTKLIDNNKTE--	KEILDAP	342
Db	1574	QGRTTQODLSALQKNSDLKLDQDDIQNRATSPATVVKDIEGPMSEENQTKLSPRELTALR	1633		
Qy	343	DKM--CSKLPKSLSEBCEQVVDYTGSSIIILIEEVSPELVCSMLHLCSGTRLPALTVVH	400		
Db	1634	EKLHQAKQEQYALQOETRVQAQKELEBAVTSALQOQETEKSKAAKEL--	AENKKKIDALLDW	1692	
Qy	401	TOPKDGFCFEVCKKLVGYLDRLNLEKNSTKQEIILAALKEGC-----	SFLPDPYQKQ	450	
Db	1693	TSVSGSG-----	GQLLTNLP--GMEQLSGASLEKALDITDGYMGVNOAPEKLDKQ	1741	
Qy	451	CDQFVAYEYBPVL	462		
Db	1742	CENMKARHOBELL	1753		

```

RESULT 6
US-10-995-561-779
; Sequence 779, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 779
; LENGTH: 5415
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-779

```

	Query Match	4.1%;	Score 113.5;	DB 6;	Length 5415;
	Best Local Similarity	16.3%;	Pred. No. 2.1;		
	Matches	80;	Conservative	88;	Mismatches 191; Indels 133; Gaps 19;
Qy	71	TAAGDMLKONATBE-----ILVLEKTCDWLPKPNNMSACKEIVDSYLVPIVL	118		
		: : :	:	:	:
Db	1295	TAAQEWMKKQABSDSVLSEQLSQTALFAEIRNOTKLDDQ-----CQFSSQQSYSTIVK	1348		
		: : :	:	:	:
Qy	119	D-----TIKGWSPRGVCNALCESLOKHAEI-----NHQKOL---	154		
		: : : :	:	:	:
Db	1349	DVELOLMTWKAFVYESQQSKPGKRMRMLSSDATALTSFMDLTRTYALTTLTTQHVKYISD	1408		
		: : : :	:	:	:

Wed Jan 18 11:58:40 2006

```

QY 155 -----BSNKIPE---LDMTEVAPFMANIPLILYPQDGRSKPQKONGDV----- 197
Db 1409 ALRLEBEEKVBEKQBHEKVKELLGWSTLARNTQKATSETSTESDIEKAILLEQQ 1468
QY 198 --CDQCMTVDIQTAVRTNSTFVQALVEH-----VKEECDRLGFGMADICKNY 244
Db 1469 VLSEBLLTKQEQVSEAIKTSQIF---LAGHGKLSSEKKEKQISQOLNALNKAYHDLCDGS 1525
QY 245 ISQYSEIAIOM-----MMMQPKBEICALVGFCDVEKEMPQTLVPAKVASK 290
Db 1526 ANOLOQLOSLAHQTEQKTLQKQNTCHQOEDLCSWVQAERA-----LAGH 1573
QY 291 NVIPALELVEPIKKEHVPK---SDVYCEVCF--LVKEVTYKLDNNKTE---KEILDAF 342
Db 1574 QRTTQODLSALQKQNSDLKQDDIQNRATSFATVVKDIEGFMENQTKLSPRELTALR 1633
QY 343 DKM--CSKLPKLSBECQEVVDYTGSSILSILLESVPELVCMSMLHLCSTGTRLPALTAVHV 400
Db 1634 EKLHOAKEQEALQEETRAVAKLEBAVTSALQOETEKSKAAKEL--AENKKKIDALLDWV 1692
QY 401 TQPKDGGFCVCKKLVGYLDRLNLEKNSTKQEIILAALEKGC-----SFLPDYQKQ 450
Db 1693 TSVGSSG-----GQLLTNLP--GMEQLSGASLEKGALDITTDGYMGVNOAPEKLDKO 1741
QY 451 CDQFVAEYEPVL 462
Db 1742 CEMKARHQBELL 1753

RESULT 7
US-10-995-561-775
; Sequence 775, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 775
; LENGTH: 5464
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-775

Query Match 4.1%; Score 113.5; DB 6; Length 5464;
Best Local Similarity 16.3%; Pred. No. 2.2;
Matches 80; Conservative 88; Mismatches 191; Indels 133; Gaps 19;

QY 71 TAAGDMLKDNATBEE-----ILVLEKTCDWLPKPNMSASCKEIVDSYLPVL 118
Db 1295 TAOQEMKPKQAEBSRVLSQLSQOTAFABIERNTQKLDQ-----CQKFSQYSTIVK 1348
QY 119 D-----IIGKMSRGEVCSALNLCESLQKHLAE-----NHQKOL-- 154
Db 1349 DYELQMTYKAFVSEQSKSPKRRRLMSSDADITQEFMDLRTYALTALVTLTQHVKYSD 1408
QY 155 -----ESNKIPE---LDMTEVAPFMANIPLILYPQDGRSKPQKONGDV----- 197
Db 1409 ALRLEBEEKVBEKQBHEKVKELLGWSTLARNTQKATSETSTESDIEKAILLEQQ 1468
QY 198 --CDQCMTVDIQTAVRTNSTFVQALVEH-----VKEECDRLGFGMADICKNY 244
Db 1469 VLSEBLLTKQEQVSEAIKTSQIF---LAGHGKLSSEKKEKQISQOLNALNKAYHDLCDGS 1525
QY 245 ISQYSEIAIOM-----MMMQPKBEICALVGFCDVEKEMPQTLVPAKVASK 290
Db 1469 VLSEBLLTKQEQVSEAIKTSQIF---LAGHGKLSSEKKEKQISQOLNALNKAYHDLCDGS 1525
QY 245 ISQYSEIAIOM-----MMMQPKBEICALVGFCDVEKEMPQTLVPAKVASK 290
Db 1526 ANOLOQLOSLAHQTEQKTLQKQNTCHQOEDLCSWVQAERA-----LAGH 1573

```

```

QY 291 NVIPALELVEPIKKEHVPK---SDVYCEVCF--LVKEVTYKLDNNKTE---KEILDAF 342
Db 1574 QRTTQODLSALQKQNSDLKQDDIQNRATSFATVVKDIEGFMENQTKLSPRELTALR 1633
QY 343 DKM--CSKLPKLSBECQEVVDYTGSSILSILLESVPELVCMSMLHLCSTGTRLPALTAVHV 400
Db 1634 EKLHOAKEQEALQEETRAVAKLEBAVTSALQOETEKSKAAKEL--AENKKKIDALLDWV 1692
QY 401 TQPKDGGFCVCKKLVGYLDRLNLEKNSTKQEIILAALEKGC-----SFLPDYQKQ 450
Db 1693 TSVGSSG-----GQLLTNLP--GMEQLSGASLEKGALDITTDGYMGVNOAPEKLDKO 1741
QY 451 CDQFVAEYEPVL 462
Db 1742 CEMKARHQBELL 1753

RESULT 8
US-11-196-400-3
; Sequence 3, Application US/11196400
; Publication No. US20050287166A1
; GENERAL INFORMATION:
; APPLICANT: DRUILHE, PIERRE
; APPLICANT: DAUBERGES, PIERRE
; TITLE OF INVENTION: MALARIAL PRE-ERYTHROCYTIC STAGE POLYPEPTIDE MOLECULES
; FILE REFERENCE: 200773US0DIV
; CURRENT APPLICATION NUMBER: US/11/196,400
; CURRENT FILING DATE: 2005-08-04
; PRIOR APPLICATION NUMBER: US/09/742,096
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 08/973,462
; PRIOR FILING DATE: 1998-02-06
; PRIOR APPLICATION NUMBER: PCT/FR96/00894
; PRIOR FILING DATE: 1996-06-12
; PRIOR APPLICATION NUMBER: FR 95/07007
; PRIOR FILING DATE: 1995-06-13
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 3
; LENGTH: 1786
; TYPE: PRT
; ORGANISM: P. falciparum
US-11-196-400-3

Query Match 4.1%; Score 113; DB 7; Length 1786;
Best Local Similarity 19.5%; Pred. No. 0.56;
Matches 94; Conservative 97; Mismatches 169; Indels 122; Gaps 27;

QY 56 PTVKSLPC-DICKDVTAAAGDMLKDNATBEEILVLEKTCDWLPKPNMSASCKE-IVDSY 113
Db 737 PTVEIIVAPSVVESVAPSVESVEEN--VEESVAENVEESV-----AENVEESVAENVEESV 791
QY 114 LPVILDIKNGSRPGEVCSALNLCESLQKHLAE---LNHQKQLESNKIPELDMTEVAP 170
Db 792 APTVEIIVAPSVVEE-----SVAPSVESVAENVATNLSNLLSGGIEETBEIKDS 843
QY 171 FMANIPLILYPQDGRSKPQKONGDVCDCTQMTVDI-----QTAVRTNSTFVQALVEH 225
Db 844 ILNEI-----BEVKN-----VVTILENVEETTAESVTFP--SNILE 880
QY 226 VKEEC---DRLGFMADICKNYSQYSEIAIOMMQPKBEICALVGFCDVEKEMPQTL 282
Db 881 IQNTTNDITIEKLEHENVLSAAL---NQSBEEKKEVIDVI---BEVKEEVATTL 934
QY 283 V-----PAKVASKNVIPALELVEPIKKEHVPKSDVYCEVCFE-----VKEBVK 327
Db 935 IETVEQAEKSAANTI--TEIFENLEENAVESNEN--AENLEKNETVNTVLDKVEETVE 991
QY 328 L-----IDNNTKEIL--DAFDK-----MCSKLPKLSBECQEVVDYTGSSILSI 371
Db 992 ISGESLENEMDAFFSEIFDNVKGIOENLLTGMFRSIETSIIVIQSBKBDLNLNVVSSI 1051
QY 372 L--LEEVSPELVCMSMLHLCSTGRL--PALTVHVTQPKDGGFCVCKKLVGYLDRLNLEKNST 428

```



```

Db      953 HLT-----LGKNEFSVS-LLNEDPKSLDIFIKAVHTTKELYAGMPTI 994
Qy      283 VPAKVASKNVIPALELVEPIKKGHEVPAKSD-----VYCE--VCEFLVKEV 325
Db      995 -----QITALEKITKPPFAAISDEKVVQOKLLRMLFDLLVNCNKHCAQTVSSV 1042
Qy      326 TYGLIDNNKTEKI-LDAFD-----KWCCKLPKSLBECQEVVDITYGS--SILSIL 372
Db      1043 FPGISVNAEQVRIELEPPDKAKPLCTVQKKRQKMQOKKSQDLBSVQGVGSYQWRVTLI 1102
Qy      373 LBEV-----SPB-LVCSMLHLCSGTRLPALTAVHTOPKGGFCVCKLVGLDRLNLE 424
Db      1103 LELLQHKKKLRSPQILVPTLFLNLSRCLFPL-----PQEG-----NWE 1141
Qy      425 KNTKQEIILAALEKGSFLPDVPQKQDCDFVAIEYEPVLEIILVYMDPSFVCLKITGACPS 484
Db      1142 --YTKQILSCLNLCOKL-SPDGGKPKDILDEKFNVELIVQ-----CIRLSEMPQ 1191
Qy      485 AHKP---LIGT 492
Db      1192 THHALLLIGT 1202

RESULT 11
US-11-124-368A-280
; Sequence 280, Application US/11124368A
; Publication No. US20050287559A1
; GENERAL INFORMATION:
; APPLICANT: Michele Cargill
; APPLICANT: James J. Devlin
; APPLICANT: May Luke
; TITLE OF INVENTION: Genetic Polymorphisms Associated with
; TITLE OF INVENTION: Vascular Diseases, Methods of Detection and Uses Thereof
; FILE REFERENCE: CL001524
; CURRENT APPLICATION NUMBER: US/11/124,368A
; CURRENT FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: US 60/568,845
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: US 60/625,936
; PRIOR FILING DATE: 2004-11-09
; NUMBER OF SEQ ID NOS: 2112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 280
; LENGTH: 2036
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-124-368A-280

Query Match 3.9%; Score 107.5; DB 7; Length 2036;
Best Local Similarity 20.0%; Pred. No. 1.8;
Matches 110; Conservative 91; Mismatches 191; Indels 159; Gaps 27;

Qy      1 MYALFLLASLL---GAALAGPV-LGLKECTRGSAVNCQVKTASDCGAVKHCLQTVWKNP 56
Db      752 VFQLEKFCVLTWYGSLSPLNCVKTVLQVALYVGCAMLSQKTKCKHQLAST--SSP 810
Qy      57 TVKSLPCDI---CKDVVTAAGDMLKDNATBEIILVLEKTCDWLPKPNMSASCKEIVDSY 113
Db      811 VVTSLLNLGSPVKEVRAA-----IQCLQALSQV 840
Qy      114 LPVILDIKGMSPRGVCS-ALNLCESLQKHLAEILNHOKLESNKIPELDMTEVVAPFM 172
Db      841 ASPFVLIIDHLISAEIITSDAAYVIQDLATLFEELQREKKLASH-----QKLSLTL 892
Qy      173 ANIPLLLYPDGPRSKQPKP-----DNGD-VCQDCIQMTVDIQTAVRTNSTFV---QALVE 224
Db      893 KNLISCVYSCPSYATKOLMKVLQVNGEWLSQLPMAEQLELEKIQKEPTAVILKDEAWVL 952
Qy      225 HVKEBCDRLPGMADICKNYISQYSEIAIOMMMQPKIECALYGFCDVEKEM--PMOTL 282
Db      953 HLT-----LGKNEFSVS-LLNEDPKSLDIFIKAVHTTKELYAGMPTI 994
Qy      283 VPAKVASKNVIPALELVEPIKKGHEVPAKSD-----VYCE--VCEFLVKEV 325

```

QY 326 TKLIDNNKTEKEI-LDAFD-----KMSCKLPKSLSEBCEQVVDITYGS--SILSIL 372
Db 1043 FKGISVNAEQVRIELEPPDKAKPLGTVQKRRQKMQQKKSQDLESQVGGSYWQVRVTLI 1102
QY 373 LEEV-----SPE-LVCSMLHLCSTGTRLPALTAVHVTQPKDGGFCEVCKKLVGYLDNRLE 424
Db 1103 LELLQHKKKLRSFQILVPTFLNLSRCLLEPL-----POEQG-----NME 1141
QY 425 KNSTKQBEILAALEKGCSTFLPDYQKQCDQFVAEYEPVLIEILVEMDPSFVCLKIGACPS 484
Db 1142 --YTKQILISCLNLCQKL-SPDGGKIPKDIIDBEKFNVELIVQ-----CIRLSEMPQ 1191
QY 485 AHKP---LLGT 492
Db 1192 THHALLLLGT 1202

RESULT 13

US-11-124-368A-278
; Sequence 278, Application US/11124368A
; Publication No. US20050287559A1
; GENERAL INFORMATION:
; APPLICANT: Michele Cargill
; APPLICANT: James J. Devlin
; APPLICANT: May Luke
; TITLE OF INVENTION: Genetic Polymorphisms Associated with
; TITLE OF INVENTION: Vascular Diseases, Methods of Detection and Uses Thereof
; FILE REFERENCE: CL001524
; CURRENT APPLICATION NUMBER: US/11/124,368A
; CURRENT FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: US 60/568,845
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: US 60/625,936
; PRIOR FILING DATE: 2004-11-09
; NUMBER OF SEQ ID NOS: 21112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 278
; LENGTH: 2044
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-124-368A-278

Query Match 3.9%; Score 107.5; DB 7; Length 2044;

Best Local Similarity 20.0%; Pred. No. 1.8;
Matches 110; Conservative 91; Mismatches 191; Indels 159; Gaps 27;

QY 1 MYALFLASLL---GAALAGPV-LGLKECTGRSAVWCQNVKTASDCGAVKHCLOTVWVWKP 56
Db 760 VFQLFKFCVSWTYGSSLSNPLNCSVKTVLTQALYVGCAMLSSQKTCQKQLASI-SSP 818
QY 57 TVKSLPCDI---CKDVTAAAGDMLKDNATEBEILVYLEKTDWLKPKNMSASCKEIVDSY 113
Db 819 VTSLLINLGSPVKEVRAA-----IQCLQALSGV 848
QY 114 LPVILDIITKEMSRPGEVCS--ALNLCESLQKHLAEHLNHOLESNKIPBLDMTEVVAPPM 172
Db 849 ASPFYLIIDHLISKABEITSDAAYVIQDLATLFEELQREKKLKH-----QKLSSETL 900
QY 173 ANIPLLLYPDGPRSKPQPK---DNGD--VCODCTQMVTDIQTAVRTNSTFV---QALVE 224
Db 901 KNLSSCVYSCPSYIAKDLMKVLLQGVNGEMVLSQLLPMAEQLEKIQKEPTAVLKDEAMVL 960
QY 225 HVKBECDRLGPGMADICKNVIISOYSEIAIOMMHMQPKIEICALVGFCDDEVKEM--PMOTL 282
Db 961 HLT-----LGKYNFVS--LLNEDPKSLDIFIKAVHTTKELYAGMPTI 1002
QY 283 VPAKASKNVIPALELVEPIKKEHVEPAKSD-----VYCE--VCEFLVKEV 325
Db 1003 -----QITALEKITKPPFAAISDEKVVQKLLRMLFDLLVNCNKHCAQTGVSSV 1050
QY 326 TKLIDNNKTEKEI-LDAFD-----KMSCKLPKSLSEBCEQVVDITYGS--SILSIL 372
Db 1051 FKGISVNAEQVRIELEPPDKAKPLGTVQKRRQKMQQKKSQDLESQVGGSYWQVRVTLI 1110

QY 373 LEEV-----SPE-LVCSMLHLCSTGTRLPALTAVHVTQPKDGGFCEVCKKLVGYLDNRLE 424
Db 1111 LELLQHKKKLRSFQILVPTFLNLSRCLLEPL-----POEQG-----NME 1149
QY 425 KNSTKQBEILAALEKGCSTFLPDYQKQCDQFVAEYEPVLIEILVEMDPSFVCLKIGACPS 484
Db 1150 --YTKQILISCLNLCQKL-SPDGGKIPKDIIDBEKFNVELIVQ-----CIRLSEMPQ 1199
QY 485 AHKP---LLGT 492
Db 1200 THHALLLLGT 1210

RESULT 14

US-11-124-368A-277
; Sequence 277, Application US/11124368A
; Publication No. US20050287559A1
; GENERAL INFORMATION:
; APPLICANT: Michele Cargill
; APPLICANT: James J. Devlin
; APPLICANT: May Luke
; TITLE OF INVENTION: Genetic Polymorphisms Associated with
; TITLE OF INVENTION: Vascular Diseases, Methods of Detection and Uses Thereof
; FILE REFERENCE: CL001524
; CURRENT APPLICATION NUMBER: US/11/124,368A
; CURRENT FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: US 60/568,845
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: US 60/625,936
; PRIOR FILING DATE: 2004-11-09
; NUMBER OF SEQ ID NOS: 21112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 277
; LENGTH: 2144
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-124-368A-277

Query Match 3.9%; Score 107.5; DB 7; Length 2144;

Best Local Similarity 20.0%; Pred. No. 1.9;
Matches 110; Conservative 91; Mismatches 191; Indels 159; Gaps 27;

QY 1 MYALFLASLL---GAALAGPV-LGLKECTGRSAVWCQNVKTASDCGAVKHCLOTVWVWKP 56
Db 860 VFQLFKFCVSWTYGSSLSNPLNCSVKTVLTQALYVGCAMLSSQKTCQKQLASI-SSP 918
QY 57 TVKSLPCDI---CKDVTAAAGDMLKDNATEBEILVYLEKTDWLKPKNMSASCKEIVDSY 113
Db 919 VTSLLINLGSPVKEVRAA-----IQCLQALSGV 948
QY 114 LPVILDIITKEMSRPGEVCS--ALNLCESLQKHLAEHLNHOLESNKIPBLDMTEVVAPPM 172
Db 949 ASPFYLIIDHLISKABEITSDAAYVIQDLATLFEELQREKKLKH-----QKLSSETL 1000
QY 173 ANIPLLLYPDGPRSKPQPK---DNGD--VCODCTQMVTDIQTAVRTNSTFV---QALVE 224
Db 1001 KNLSSCVYSCPSYIAKDLMKVLLQGVNGEMVLSQLLPMAEQLEKIQKEPTAVLKDEAMVL 1060
QY 225 HVKBECDRLGPGMADICKNVIISOYSEIAIOMMHMQPKIEICALVGFCDDEVKEM--PMOTL 282
Db 1061 HLT-----LGKYNFVS--LLNEDPKSLDIFIKAVHTTKELYAGMPTI 1102
QY 283 VPAKASKNVIPALELVEPIKKEHVEPAKSD-----VYCE--VCEFLVKEV 325
Db 1103 -----QITALEKITKPPFAAISDEKVVQKLLRMLFDLLVNCNKHCAQTGVSSV 1150
QY 326 TKLIDNNKTEKEI-LDAFD-----KMSCKLPKSLSEBCEQVVDITYGS--SILSIL 372
Db 1151 FKGISVNAEQVRIELEPPDKAKPLGTVQKRRQKMQQKKSQDLESQVGGSYWQVRVTLI 1210
QY 373 LEEV-----SPE-LVCSMLHLCSTGTRLPALTAVHVTQPKDGGFCEVCKKLVGYLDNRLE 424

Db	1211	LELLQHKKLRSPQILVPTLFNLLSRCL	EP-----PQEQ-----NME	1249
Qy	425	KNSTKQBIILAELKGCSEFLDPDPYKQCDQFVAEYEPVLIELVLVEMDPSPVCLKIGACPS		484
Db	1250	--YTKQLILSCLLNICOKL--SPDGGKIPKOILDEEKFNVLELIVQ-----CIRLSEMPQ		1299
Qy	485	AKP---LIGT	492	
Db	1300	THHALLLGLT	1310	

```

RESULT 15
US-11-196-400-5
; Sequence 5, Application US/11196400
; Publication No. US20050287166A1
; GENERAL INFORMATION:
; APPLICANT: DUILHE, PIERRE
; APPLICANT: DAUBERSIES, PIERRE
; TITLE OF INVENTION: MALARIAL PRE-ERYTHROCYTTIC STAGE POLYPEPTIDE MOLECULES
; FILE REFERENCE: 200773USDIV
; CURRENT APPLICATION NUMBER: US/11/196,400
; CURRENT FILING DATE: 2005-08-04
; PRIOR APPLICATION NUMBER: US/09/742,096
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 08/973,462
; PRIOR FILING DATE: 1998-02-06
; PRIOR APPLICATION NUMBER: PCT/FR96/00894
; PRIOR FILING DATE: 1996-06-12
; PRIOR APPLICATION NUMBER: FR 95/07007
; PRIOR FILING DATE: 1995-06-13
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5
; LENGTH: 630
; TYPE: PRT
; ORGANISM: P. falciparum
US-11-196-400-5

```

Query Match	3.7%	Score 102;	DB 7;	Length 630;
Best Local Similarity	18.1%	Prod. No. 1.1;		
Matches	74;	Conservative 103;	Mismatches 155;	Indels 76; Gaps 21;
QY	56	PTVKSLPDCIDKDVTTAAGMLKDN---ATEEEIILVLEKT-----CDMLPKPNMSASCKE	108	
DB	172	PTVEEI---VAPSVESVAPSVESVAPSVESVAENVEEIVAPSVESVAE	228	
QY	109	IVDSYLPVLIDIIKGMSPRGVCSALNLCESIQKHILAHNKHOKLESNKIPELDMTEVV	168	
DB	229	NVEE---SVAENVEESVAENVEESVAENVEEIVAPTVESVATVE---EIV	282	
QY	169	APFM-----ANIPLLYLPQDGRPKQPKDNGDVQCDCIQMYTD-IQTAVRTNSTFVQAL	222	
DB	283	APTVEESVAPTVEEIVPVSVEESVAPSVES--VAENVEESVAENVEESVAEN--VEESV	338	
QY	223	VEHVKEEC-----DRLPGMGADICKNVISQYSIAIQMMHMQPKKEICALVG--FCDVEK	275	
DB	339	AENVEESVAENVEEIVAPSVESVAPTVEE--SVAENVATNLSNDLNLNLGGIETEEK	396	
QY	276	EMPMQTLVPKAVASKNWIPIA-LELVBPICKGHEVPKASDVYCEVCFVLKVEVTKLIDNNKT	334	
DB	397	DSIINBIEEVK---ENVVTILEKVEETAEVSVTFTSNILEEQ-----NTITNDTI	446	
QY	335	EKEILDAPDKMCKLPSKL--SEFCQEVVDTYGSIIILLESVEVSVELVCSMLHLCSGTR	392	
DB	447	EKLEELHENVLSAALENTQSEEEKCEVID-----VIEEVKEEVATLLIE-----	491	
QY	393	LPALTIVHTQPDGGFCVCKKLGYILDRNLKNS--TKOEIIAALAEK	438	
DB	492	-----TVEQAE-----SESSSTTETEPENLEENAVESNEKVAENLEK	528	

Search completed: January 13, 2006, 16:39:05
Job time : 12.4106 secs

**This Page is Inserted by IFW Indexing and Scanning
Operations and is not part of the Official Record**

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images include but are not limited to the items checked:

☐ BLACK BORDERS

☒ IMAGE CUT OFF AT TOP, BOTTOM OR SIDES

☐ FADED TEXT OR DRAWING

☐ BLURRED OR ILLEGIBLE TEXT OR DRAWING

☐ SKEWED/SLANTED IMAGES

☐ COLOR OR BLACK AND WHITE PHOTOGRAPHS

☐ GRAY SCALE DOCUMENTS

☐ LINES OR MARKS ON ORIGINAL DOCUMENT

☒ REFERENCE(S) OR EXHIBIT(S) SUBMITTED ARE POOR QUALITY

☐ OTHER: _____

IMAGES ARE BEST AVAILABLE COPY.

As rescanning these documents will not correct the image problems checked, please do not report these problems to the IFW Image Problem Mailbox.

THIS PAGE BLANK (USPTO)